Mouse ant Human tra Anti-TNFa Anti-TNFa Remicade

Human ant Human tra Chimeric

Monoclona B-B10 MAb Anti-NKG2 Anti-NKG2 Humanised OC125-3.1 Protein u Mrcin Tn Frotein u Excesin u

Adf89616 Adh89387 Adi70798 Abr55861 Abr55861 Adh49714 Adh49714 Adh4977610 Aar37610 Aar37610

Human p53 Monoclona

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An anti-TNF chimeric antibody may be administered for treating TNF-alpha mediated Crohn's disease in a human. The anti-TNF chimeric antibody competitively inhibits binding of TNF to monoclonal antibody CA2. The anti-TNF antibody does not bind to one or more epitopes in amino acids 11 37, 47, 49-57 or 155-157 of hTNF, but does bind to one or more epitopes included in amino acids between 87-108 or both 87-108 and 59-80 of hTNF. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INF; tumour necrosis factor; Crohn's disease; cA2 antibody.
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ADF89616
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(UYNY-) UNIV NEW YORK MEDICAL CENT.
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92US-00853606.
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  WPI; 1997-414547/38.
N-PSDB; AAT87441.
                                                         04-FEB-1994;
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12-JAN-1998
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11-SEP-1992;
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02-FEB-1993;
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361,932 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Treatment of tumor necrosis factor-alpha mediated disease using chimeric
invention for alleviating symptoms or pathologies involving TNF, such as bacterial, viral or parasitic infections, chronic inflammatory diseases, autoimmune diseases, malignancies and/or neurodegenerative diseases
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                                                                                                                                                                                                                                                                                 1 DILLTQSPAILSVSPGERVSFSCRASQFVGSSIHWYQQRTNGSPRLLIKYASESMSGIPS
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TNF-alpha mediated disease; anti-TNF chimeric antibody;
monoclonal antibody cA2; autoimmune disease; inflammatory disease;
neurodegenerative disorder; cerebalar cortical degeneration;
multiple system degeneration; multi-system disorder; Senile Dementia;
amyotrophic lateral sclerosis; spinal muscular atrophy;
Alzheimer's disease; Down's Syndrome; Diffuse Lewy body disease;
Wernicke-Korsakoff syndrome; chronic alcoholism;
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                                                                                                                                            100.0%; Score 557; DB 2;
100.0%; Pred. No. 8.6e-38;
iive 0; Mismatches 0;
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UNIV NEW YORK STATE.
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Matches 107; Conservative
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N-PSDB; AAX81705.
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11-SEP-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumour necrosis factor; human; hTNF; rheumatoid arthritis; malignancy; anti-TNF chimmeric anti-Lhody; inhlbitor; therapy; diagnosis; infection; chronic inflammatory disease; autoimmume disease; light chain; neurodegenerative disease; variable region.
                                                                                                                                                 DILLIQSPAILSVSPGERVSFSCRASQFVGSSIHWYQQRTNGSPRLLIKYASESMSGIPS
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                                                                                                      Indels
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                                                       100.0%; Score 557; DB 2; 100.0%; Pred. No. 8.6e-38;
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                                                                                                      Mismatches
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(UYNY-) UNIV NEW YORK MEDICAL CENT.
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N-PSDB; AAV03615.
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107; Conserv
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04-FEB-1994
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                                                    Query Match
Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW40820;
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                                                                                                         Matches
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AAM 40
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Vilcek J;

Seigal S,

98US-00133119

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12-AUG-1998;
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chimeric antibodies are useful for treating and/or diagnosing TNF-alpha mediated diseases such as immune and autoimmune pathologies e.g. rheumatoid arthritis and especially systemic lupus erythematosus (SIEB), thyroidosis, graft versus host disease, caleroderma, diabetes mellitus, and Graves' disease; inflammatory diseases (other than septic shock), neurodegenerative disorders, cerebellar cortical degenerations, miltiple systems degenerations (e.g. Mencel, Dejerine-Thomas, Shi-Drager, and Machado-Joseph), Refsum's disease, abetalipoprotemia, ataxia, telangiectasia, mitcohondrial multi-system disorder, amyotrophic lateral celerosis, infantile and juvenile spinal muscular atrophy, Alzheimer's disease, Down's Syndrome in middle spen Diffuse Lewy body disease, Senile Dementia of Lewy body type, Wernicke-Korakoff syndrome, chronic alcoholism, Creutzfeldt-Jakob disease, sub-acute sclerolising panencephalitis, Hallerroaden-Spatz disease, dementa pugalistica, lumphomas, other TNF-secreting tumors or alcohol-induced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, tumour necrosis factor-alpha, TNF-alpha, chimeric antibody, immunoglobulin, inflammation, cancer; cachexia, sepsis; endotoxic shock; infection, chronic inflammatory disease, auto-immune disease, malignancy, neurodegenerative disease, crohn's disease; rheumatoid arthritis, A2; vascular endothelial growth factor; VEGF, VEGF-mediated disease.
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                                                                                                                                                                                                                                  Length 107;
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                                                                                                                                                                                                                                 100.0%; Score 557; DB 2;
100.0%; Pred. No. 8.6e-38;
iive 0; Mismatches 0;
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92US-00853606.
92US-00943852
93US-00010406.
94US-00192103.
94US-00192103.
94US-00192861.
94US-00192861.
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Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                            Sequence 107 AA;
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Homo sapiens.
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18-MAR-1992;
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02-FEB-1993
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11-DEC-1995
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                                                                                                                                                                                     hepatitis
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The present sequence represents the light chain variable region of a chimeric human-murine A2 antibody (cA2) which binds to epitopes of human tumour necrosis factor (TNP)-alpha. Chimeric antibodies of the invention comprise at least part of a human immunoglobulin constant region and at least part of a non-human immunoglobulin variable region. The chimeric antibodies are useful in vivo diagnosis and therapy of TNF-alpha-mediated pathologies and conditions. They can also neutralize human TNF-alpha-mediated pathologies and conditions. This is useful as TNF is known to be under physiological conditions. This is useful as TNF is known to be involved in e.g. pro-inflammatory actions, wasting associated with cancer and other diseases (cachexia), gram-negative sepsis and endotoxic shock. Antibodies can be used to treat and/or disgnose bacterial, parasitic or viral infections, chronic inflammatory diseases (such as crobn's diseases of rheumatoid arthritis). As inhibition or antagonism of TNF also decreases the expression of vascular endothelial growth factor (VEGF), the cathodies are also useful to treat VEGF-mediated diseases. (Updated on 1-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                            New chimeric antibody binding an epitope specific for human tumor necrosis factor alpha useful in treatment and diagnosis of tumor necrosis factor alpha related conditions e.g. Crohn's disease.
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                                                                   Siegel
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                                                                   Knight D,
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100.0%; Pred. No. 8.6e-38;
iive 0; Mismatches 0;
                                                                   Ghrayeb J,
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                                                                       Daddona
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(CENZ ) CENTOCOR INC.
                                                                                                                                       2001-615872/71.
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Best Local Similarity
                                                                       Vilcek J,
                                                                                                                                                                                N-PSDB; AAI65695
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                                                                           Le J,
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ABG70572 standard; protein; 107 AA
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Matches
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                                                                                                                                                                                                                                                                               The invention relates to chimeric anti-tumour necrosis factor (TNF)
antibodies. These chimeric antibodies comprises two light chains and two
heavy chains, each of the chains comprises two light chains and two
immunoglobulin (Ig) constant region and at least part of a human
immunoglobulin (Ig) constant region and at least part of a non-human go
variable region, where the antibodies are capable of binding an epitope
specific for human TNF-alpha. Anti-TNF antibodies or peptides may be used
in research, therapeutic and diagnostic methods, specifically for
cinditions associated with the presence of a substance reactive with an
anti-TNF antibody. TNF-related pathologies include acute and chronic
immune and autoimmune disorders (e.g. systemic lupus erythematosus,
theuwatoid arthritis, infections (e.g. bacterial, viral, fungal or
parastic infections), inflammatory diseases (e.g. ulcerative colitis,
conditions associated seed on the based ganglia or cerebellar
disorders), malignant pathologies (e.g. leukaemia, lymphomas), or alcohol-
induced hepatitis. The anti-TNF peptide or antibodies may also be used
for immunoassays, which derect or quantitate TNF or anti-TNF antibodies.
The present sequence is mouse light chain variable region of chimeric A2
anti-TNF antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, tumour necrosis factor, TNF, anti-TNF antibody, cA2; infection, sepsis; cachexia, acquired immunodeficiency syndrome, AIDS, septic shock, chronic inflammatory disease; disseminated intravascular coagulation, atherosclerosis; ulcerative colitis; chronic inflammatory bowel disease, autoimmune disease; rheumatoid arthritis; diabetes mellitus; graft versus host disease; Grave's disease; alcohol-induced hepatitis;
                                                                                                                                                                                                     Chimeric anti-tumor necrosis factor (TNF) antibodies useful for diagnosing or treating TNF-associated pathologies or conditions, e.g. chronic and acute immune, autoimmune disorders, and microbial infections.
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                                                                                                                                    Siegel SA;
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                                                                                                                                    Knight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 557; DB 4;
100.0%; Pred. No. 8.6e-38;
iive 0; Mismatches 0;
                                                                                                                                    Ghrayeb J,
                                                                                           NEW YORK MEDICAL CENT
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                       92US-00853606.
92US-00943852.
93US-00010406.
93US-00013413.
                                                                                                                                    Dadonna P,
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107; Conservative
                                                                                                                                                              2001-595467/67.
                                                                                           UNIV NEW
                                                                                                                                    Vilcek J,
                                                                                                                                                                            N-PSDB; AAD18192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 107 AA;
                        18-MAR-1992
                                        11-SEP-1992,
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Best Local S
                                                                                          (CENZ )
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The present sequence represents the cloned light chain variable region of antibody cA2, which is directed against tumour necrosis factor (TNF). The specification describes anti-TNF antibodies, such as cA2. The anti-TNF caltibody is useful for alleviating symptoms or pathologies involving TNF, such as bacterial, viral or parasitic infections (e.g. sepsis, cachexia, acquired immunodeficiency syndrome (AIDS) and septic shock), chronic inflammatory diseases (diseaseintated intravascular coagulation, atherosclerosis, ulcerative colitis and chronic inflammatory bowel disease), autoimmune disease (e.g. rheumatory bowel disease), autoimmune disease (e.g. rheumatory disease), alcohol-induced healtits, antignancies and/or neurodegenerative disease), alcohol-induced calticis, damignancies and/or neurodegenerative diseases (e.g. multiple sclerosis, demyelinating diseases and acute transverse myelitis). The antibody is also useful in the treatment of vascular endothelial cowth factor (VEGE) mediated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecule encoding heavy or light chain variable regions of anti-tumor necrosis factor antibody, useful for alleviating symptoms or pathologies involving tumor necrosis factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Siegel S;
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malignancy; neurodegenerative disease; multiple sclerosis; demyelinating disease; acute transverse myelitis; vascular endothelial growth factor-mediated disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 557; DB 4; Length 1
100.0%; Pred. No. 8.6e-38;
ive 0; Mismatches 0; Indels
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UYNY-) UNIV NEW YORK MEDICAL CENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                             91US-00670827.
92US-00853606.
92US-00943852.
93US-00013413.
94US-00192093.
94US-00192861.
94US-00192861.
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nes 107; Conservative
                                                                                                          VEGF-mediated disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-588928/66.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH78592
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                                                                                                                                                                                                                                   US6277969-B1
                                                                                                                                                                                                                                                                                                                                                                      12-AUG-1998;
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29-JAN-1993;
02-FEB-1993;
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18-OCT-1994;
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18-MAR-1992
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(first entry)

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Disclosure, Fig 16A; 95pp; English
                                                                                                   18-JAN-2001; 2001US-00766535
                                                                                                                                                    (CENZ ) CENTOCOR INC.
                                                                                                                                                                 WPI; 2002-706216/76.
N-PSDB; ABS54256.
                                                                                      US2002106372-A1.
                                                                                                                                                                                   or its fragment
                                                                                                                                      18-OCT-1994;
11-DEC-1995;
12-AUG-1998;
                                                                     Homo sapiens
                                                                                                                            04-FEB-1994;
                                                                                                                               04-FEB-1994;
      28-NOV-2002
                                                                                                              18-MAR-1992
                                                                                                                     29-JAN-1993
02-FEB-1993
                                                                        Mus sp.
Synthetic.
Chimeric.
                                                                                             08-AUG-2002
                                                                                                                  11-SEP-1992
                                                                                                                                                           Le J,
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91US-00670827. 92US-00853606. 92US-00094382. 93US-00013413. 94US-00192093. 94US-00192861.

Ghrayeb J,

Vilcek J, Daddona P,

95US-00570674 98US-00133119

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disorder, acute transverse myelitisa, a disorder of the motor unit, a neurogenic muscular atrophy, anterior horn cell degeneration, amyotrophic lateral scdlerosis, infantile spinal muscular atrophy, Juvenile spinal muscular atrophy, Alzheimer's disease, Down's Syndrome, a diffuse Lewy body disease, senile dementia of Lewy body type, Wernicke-Korsakoff syndrome, chronic alcoholism, Creutzfeldt-Jakob disease, subacute sclerosing panencephalitis, Hallervorden-Spatz disease, or dementia puglistica). The present sequence represents human-murine chimeric antihuman INFalpha (hINFalpha) chimeric A2 (CA2) light chain variable region. The cA2 monoclonal anti-INF antibody consists of mouse (from female Balb, c mice) antihuman INF 1921 antibody (designated A2), and the constant regions of human IgG1 kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour necrosis factor; monoclonal antibody; chimeric antibody; antibody;
myelodysplastic syndrome; cytostatic; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 557; DB 5; Length 107; 100.0%; Pred. No. 8.6e-38; ive 0; Mismatches 0; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGTDFTLSINTVESEDIADYYCQQSHSWPFTFGSGTNLEVK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESGSGSGTDFTLSINTVESEDIADYYCQOSHSWPFTFGSGTNLEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine anti-TNF antibody light chain variable region.
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92US-00853606.
92US-00943852.
93US-00010406.
94US-00192093.
94US-00192861.
94US-00192861.
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2001US-00756398
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Matches 107; Conservative
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N-PSDB; ABV73814.
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                                                                                                                                                                                                                                                                                                                                             Sequence 107 AA;
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04-FEB-1994;
04-FEB-1994;
04-FEB-1994;
18-OCT-1994;
11-DEC-1995;
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antibodies, and anti-TNF peptides, which are specific for human tumour
creasis factor-alpha (TNFalpha). Methods of producing and using the anti-
rNF antibodies and anti-TNF peptides are also disclosed. The anti-TNF
antibodies, anti-TNF peptides and methods of the invention are useful for
treating human neurodegenerative diseases (e.g. multiple sclerosis,
acquired immunodeficiency syndrome (AIDS) dementia complex, a
demyelinating disease, acute transverse myelitis, an extrapyramidal
disorder, a cerebellar disorder, a lesion of the corticospinal system, a
disorder of the basal ganglia, a hyperkinetic movement disorder,
thurington's cholera, a senile cholera, a drug-induced movement disorder,
thypokinetic movement disorder, Parkinson's disease, progressive
supranuclear palsy, a structural lesion of the cerebellum, a
spinocerebellar degeneration, spinal ataxia, Friedreich's ataxia, a
cerebellar cortical degeneration, a multiple systems degeneration, a
systemic disorder, Refsum's disease, abetalipoprotaemia, ataxia
telanglectasia, a mitochondrial multi-system disorder, demyelinating core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating a neurodegenerative disease, especially multiple sclerosis, comprises administering an anti-tumor necrosis factor monoclonal antibody
                                                                                                                                                             Human, tumour necrosis factor-alpha; TNRalpha; anti-TNF antibody; anti-TNF peptide; neurodegenerative disease; multiple sclerosis; acquired immunodeficiency syndrome; AIDS; demyelinating disease; acute transverse myelitis; extrapyramidal disorder; lesion; cerebellar disorder; basal ganglia disorder; Huntington's cholera; movement disorder; senile cholera; Parkinson's disease; spinal ataxia; progressive supranuclear palsy; spinocerebellar degeneration; systemic disorder; neurogenic muscular atrophy; Down's Syndrome; amyotrophic lateral sclerosis; Alzheimer's disease; chronic alcoholism; cetuffeldt-Jakob disease; Hallervorden-Spatz disease; neuroprotective; antiparkinsonian; human TNPalpha; hTNPalpha; antihuman TNF IgG1 antibody; IgG1 kappa; mutein.
                                                                                                                     Human-murine chimeric anti-hTNFalpha cA2 light chain variable region.
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                       The present sequence is the protein sequence of the light chain variable region (VI) of an anti-human tumour necrosis factor (TMP) monoclonal antibody (WAb) produced by maintime hybridoma line A2. A claimed method of treating a myelodysplastic syndrome in a human comprises administering an anti-TMP chimeric antibody comprising the murine A2 VL and VH (see ABPS4871) regions and an IgG1 human constant region. The anti-TMP peptides and antibodies of the invention can be used in the treatment of TMF-related pathologies such as acute and chronic immune and autoimmune pathologies, inflammatory diseases, neurodegenerative diseases, malignant pathologies, and alcohol-induced hepatitis
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                                                                                                                                                                                                                                                                                                                                                             necrosis factor; TNF; chimeric; antibody; cA2; psoriasis;
                                                                                                                                                                                            1 DILLIQSPAILSVSPGERVSFSCRASQFVGSSIHWYQQRTNGSPRLLIKYASBSMSGIPS
                                                                                                                                                                              1 DILLIQSPAILSVSPGERVSFSCRASQFVGSSIHWYQQRINGSPRLLIKYASESMSGIPS
                                                                                                                                                             Gaps
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                                                                                                                                           Length 107;
                                                                                                                                                                                                                RFSGSGSGTDFTLSINTVESEDIADYYCQQSHSWPFTFGSGTNLEVK 107
                                                                                                                                                                                                                                 61 RFSGSGSGTDFTLSINTVESEDIADYYCQOSHSWPFTFGSGTNLEVK 107
                                                                                                                                                             0; Indels
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                                                                                                                                           100.0%; Score 557; DB 5; 100.0%; Pred. No. 8.6e-38;
                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                            AAB47941 standard; protein; 107 AA
       Claim 7; Page 56; 97pp; English.
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92US-00853606.
92US-00014065.
93US-00013413.
94US-00192093.
94US-00192661.
94US-00324799.
95US-0057674.
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                                                                                                                                                                                                                                                                                                                 (revised)
(first entry)
                                                                                                                                                  al Similarity 100.
107; Conservative
                                                                                                                                                                                                                                                                                                                                           Chimeric antibody, cA2
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N-PSDB; AAI72609.
                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin; G1
                                                                                                                         Sequence 107 AA;
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                                                                                                                                                                                                                                                                                                                                                             Human; tumour
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10-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                 musculus
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                                                                                                                                                                                                                                                                                                AAB47941;
                                                                                                                                                                                                                61
                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric
                                                                                                                                                    Local
                                                                                                                                                            Matches
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                                                                                                                                                                                                    The sequences given in AAB47941-42 show the light and heavy chain variable regions of the chimeric antibody, CA2. CA2 is an anti-tumour necrosis factor (TNF) antibody. Anti-human TNF chimeric antibodies, may be used for treating psoriable in humans. Psoriable may be treated by administering: (a) anti-TNF chimeric antibody (Ab) which competitively inhibits binding of TNF to monoclonal chimeric Ab CA2; or (b) anti-TNF chimeric Ab CA2; or (b) anti-TNF chimeric Ab cap; or (b) anti-TNF chimeric Ab; or or both 59 - 80 and 87 - 108 of a TNF sequence. The CA2 antibody has potent TNF-inhibiting and/or neutralizing activity. Levels of CA2 as low as 125 ng/ml completely abolished the toxic activity of TNF. The CA2 exhibited greater TNF-inhibiting activity and/or neutralizing activity than did the parent murine A2 monoclonal antibody. (Updated on 29-AUG-2003 to standardise OS field)
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Treating psoriasis in humans comprises administering anti-tumor necrosion factor (TNF) chimeric antibody cA2, or anti-TNF chimeric antibody which competitively inhibits binding of TNF to the antibody cA2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU09889 standard; protein; 107 AA
                                                                                                                                               Claim 7; Fig 16A; 97pp; English.
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920S-00853605.
930S-00010406.
930S-00013413.
940S-00192102.
940S-00192861.
940S-00324799.
950S-00570674.
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nes 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 107 AA;
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02-FEB-1993;
04-FEB-1994;
04-FEB-1994;
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12-AUG-1998;
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11-SEP-1992;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; tumour necrosis factor; TNF; antibacterial; immunosuppressive; tumour necrosis factor inhibitor; bacterial infection; cA2; sepsis; endothelial damage; vascular damage; severe hypotension; disseminated intravascular caquiation; shock; inflammation; bacteraemia; chimeric A2 antibody; cA2; light chain varaible region.
                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid molecule that encodes a tumour necrosis factor-alpha (TNR-alpha) specific antibody. The nucleic acid molecule is useful in diagnosing and/or treating TNR-alpha-mediated pathologies and conditions, such as bacterial, viral or parasitic infections, chronic inflammatory diseases (e.g. rheumatoid arthritis, cronn's disease or ulcerative collish, Jautoimmune diseases (e.g. systemic lupus erythematosus, diabetes mellitus or Grave's disease), malignancies, vascular diseases and/or neurodegenerative diseases (e.g. Halbelmer's disease) and in research purposes. The present sequence represents the amino acid sequence of the mouse TNR-alpha antibody GAZ light chain variable region
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                                                                                                                                                  New nucleic acid molecule for diagnosing or treating tumor necrosis factor alpha-mediated diseases, e.g. infections, chronic inflammatory diseases, autoimmune diseases, cancer or neurodegenerative diseases.
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                                         Siegel S;
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                                         Ghrayeb J, Knight D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 557; DB 6;
100.0%; Pred. No. 8.6e-38;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                        Claim 4; Fig 16A; 100pp; English.
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92US-00853606.
92US-00010406
93US-00013413.
94US-00192093.
94US-00192861.
94US-00192861.
                                       Vilcek J, Daddona P,
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Matches 107; Conservative
(CENZ ) CENTOCOR INC.
                                                                                   2003-401678/38.
                                                                                                      N-PSDB; ACA61152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 107 AA;
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04-FEB-1994;
18-OCT-1994;
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02-FEB-1993;
04-FEB-1994;
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                                         Le J,
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Mouse, TNFalpha; humanised antibody; tumour necrosis factor-alpha;
antigen, constant region; heavy chain; light chain;
antigen indingr region; complementarity determining region; CDR; A2; CA2;
W framework region; cytokine; TNF; pro-inflammatory; tissue injury;
proceedulant; vascular endothelial cell; neutrophil; lymphocyte;
W procedulant; vascular endothelial cell; neutrophil; lymphocyte;
W autoimmune disorder; macrophage; lumune disorder; scleroderma;
W autoimmune disorder; rheumatoid arthritis; thyroidosis; diabetes;
W inflammatory disease; garcoidosis; chronic inflammatory bowel disease;
W neurodegenerative disease; miliphe sclerosis; Parkinson's disease;
W neurodegenerative disease; multiple sclerosis; Parkinson's disease;
W Alzheimer's disease; cancer; hepatitis; coular neovascularisation;
W soriasis; duodenal ulcer; angiogenesis; female reproductive tract;
W neuroprotective; nootropic; cytostatic; gynecological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a method of treating bacterial infection in a human comprising administering to the human a tumour necrosis factor (TNP). Inhibiting amount of an anti-TNF chimeric antibody, which competitively inhibite binding of TNF to monoclonal antibody cA2 methods are useful for treating bacterial infections, a pathology associated with a sepsis (e.g. endothelial damage, vascular damage, issulting from bacterial infection, or inflammacory reaction resulting from bacterial infection, or inflammatory reaction form of pharmacoutical and/or diagnostic compounds are useful for diagnosing an treating TMP-related pathologies. This is the amino acid sequence of the chimeric A2 (CA2) antibody light chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating bacterial infection in a human comprises administering to the human a tumor necrosis factor (TNF)-inhibiting amount of an anti-TNF chimeric antibody, which competitively inhibits binding of TNF to
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                                                                                                                                                                                                                                                                                                                                                                              Ghrayeb J,
                                                                                                                                                                                                                (UYNY-) UNIV NEW YORK MEDICAL CENT. (CENZ ) CENTOCOR INC.
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11-DEC-1995; 95US-00570674.
12-AUG-1998; 98US-00133119.
12-AUG-2001; 2001US-00957703.
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Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        monoclonal antibody cA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-174129/17.
N-PSDB; ABX14786.
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and

CA2;

ABG75773;

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The invention discloses a new humanised antibody, or its antigen-binding fragment, that selectively binds human tumour necrosis factor-alpha at least a portion of an antibody of human origin. The antibody consists of a constant region heavy or light chain of human origin and an antigen binding region. Gomprising complementarity determining regions (CDRs) derived from an antibody of murine origin. The antibody consists of the front and antibody of murine origin that binds to human The alpha (A2 or CA2), and a framework region derived from a heavy or light chain of human origin. Also disclosed is an expression vector comprising a fused gene encoding the humanised antibody, or its antigen-binding fragment, and the method for preparing it. The cytokine TNF causes pro-inflamentory actions which result in tissue injury, such as inducing procoagulant activity on vaccular endothelial cells, increasing the adherence of neutrophis and lymphocytes and stimulating the release of platelet activating factor from macrophages, neutrophils and vascular endothelial cells. The methods are useful for preparing a humanised antibody, and antigen-binding fragment, and manufacturing a polypeptide. The methods are useful for the diagnosis and treatment of TNF-related pathologies, such as acute and chronic immune and autoimmune disorders (theumacoid arthitis, thyroidosis, graft versus of inclement of file macrophy diseases, scleroderma, diabetes and Graw's diseases (sarcoidosis, chronic inflammatory bowel disease, ulcerative colities, Cronic and allowed the sease of the plate of the collegent of the col
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New humanized anti-TNF antibody with an antigen binding region, useful for diagnosing and treating TNF-related pathologies, such as autoimmune disorders, bacterial and viral infections, inflammatory diseases, AIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTDFTLSINTVESEDIADYYCQQSHSWPFTFGSGTNLEVK 107
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Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J, Vilcek J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABX11349
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                                                                                   US2002132307-A1.
Mus musculus.
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ABG75773
ID ABG75
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ABG75773 standard; protein; 107 AA.

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The invention discloses a method for treating ankylosis, by administering a tumour necrosis factor (TNF)-inhibiting anti-TNF chimeric antibody which competitively inhibites binding of TNF to the murine monoclonal antibody ca2, where the antibody comprises an immunoglobulin (Ig) Gl constant region and binds to an epitope of human TNF. The antibody constant region heavy or light chain of human origin and an antigen binding region, comprising complementarity determining regions consists of a constant region heavy or light chain of human origin and an antigen binding regions (CDRs) derived from an antibody of murine origin that binds to human crime and the framework region derived from a heavy or light chain of human origin. The cytokine TNF causes pro-inflammatory actions which result in tissue injury, such as inducing procoagulant actions which result in tissue injury, such as inducing procoagulant activity on vascular endothelial cells, increasing the adherence of neutrophils and lymphocytes and stimulating the release of platelet activating factor from macrophages, neutrophils and vascular endothelial cells. The methods and compositions are also useful for the diagnosis and creatment of ankylosis and TNF-related pathologies, such as acute and chronic immune and autoimmune disease, scleroderma, diabetes and Grave's thyroidosis, graft versus host disease, scleroderma, diabetes and Grave's
                                                                                                             Mouse, tumour necrosis factor alpha; TNFalpha; rheumatoid arthritis; TNF inhibitor; ankylosis; anti-TNF antibody; cA2; immunoglobulin G1; G1; TNF; heavy chain; light chain; antigen binding; CDF, complementarity determining region; framework region; cytchine; pro-inflammatory; tissue injury; procoagulant; vascular endothelial neutrophil; lymphocyte; platelet activating factor; macrophage; immune disorder; autoimmune disorder; rheumatoid arthritis; flyroidosis; graft versus host disease; scleroderma; diabetes; Grave's disease; chronic inflammatory bowel disease; acroidosis; chronic inflammatory bowel disease; ancoidosis; parkinson; disease; dementia Alzheimer's disease; cancer; hepatitis; coular neovascularisation; psoriasis; duodenal ulcer; anglogenesis; female reproductive tract; haemodynamic; febrile; allergic episode.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating ankylosis in a human, comprises administering a tumor necrosis factor (TNF)-inhibiting amount of anti-TNF chimeric antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Siegel S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Knight D,
                                                                              cA2 variable light chain of the TNFalpha antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Daddona P, Ghrayeb J,
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920S-00943852.
930S-00010406.
930S-00102093.
940S-00192861.
940S-00192861.
950S-00570674.
980S-0010S-00576674.
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                                       (first entry)
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N-PSDB; ABX11365.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
                                       29-APR-2003
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disease), bacterial and viral infections including AIDS, inflammatory diseases (sarcoidosis, chronic inflammatory bowel disease, ulcerative colitis, Crohn's disease and atherosoflerosis), neurodegenerative diseases (multiple sclerosis, Parkinson's disease, dementia and Alzheimer's disease), cancer, hepatitis, ocular neovascularisation, psoriasis, duodenal ulcers and angiogenesis of the female reproductive tract. The chimeric anti-TNP Mab was well-tolerated and involved no haemodynamic, febrile or allargic episodes. The sequence presented is the murine cA2 variable light chain of the TNPalpha antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   particularly a cachexia associated with cancer, HIV ninistering a tumor necrosis factor (INF)-inhibiting rine anti-TNF chimeric antibodies.
                                                                                                                                                                                                                           1 DILLIQSPAILSVSPGERVSFSCRASQFVGSSIHWYQQRTNGSPRLLIKYASESMSGIPS
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                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse; tumour necrosis factor alpha; INF alpha; immunomodulator; INF-Antagonist; cachexia; cancer; HIV; AIDS; cA2 light chain variable region.
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                                                                                                                                                                                                                                                                                                       RESGSGGTDFTLSINTVESEDIADYYCQQSHSWPFTFGSGTNLEVK 107
                                                                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLSINTVESEDIADYYCOOSHSWPFTFGSGTNLEVK 107
                                                                                                                                                                      Length 107;
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                                                                                                                                                                     Match 100.0%; Score 557; DB 6; Local Similarity 100.0%; Pred. No. 8.6e-38; les 107; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse cA2 light chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ing cachexia, particularly comprising administering a nt of human-murine anti-TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                                                                                                                                                                      ABU63587 standard; protein; 107
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92US-00853606.

92US-00010406.

93US-0013413.

94US-01192093.

94US-01192861.

94US-00192861.

94US-00192861.

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94US-00192861.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                             Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-FEB-1993;
04-FEB-1994;
04-FEB-1994;
04-FEB-1994;
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                                                                                                                                                                         Query Match
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Matches
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The invention describes a method of treating cachexia in a human comprising administering a tumour necrosis factor (TNF) inhibiting amount of: (a) an anti-TNF chimeric antibody, which competitively inhibits binding of TNF to menocional attribody (mAD) cAZ; (b) chimeric anti-TNF antibody cAZ; (c) at least one mAD cAZ, or its TNF-binding fragment; or (d) an anti-TNF chimeric antibody with epitopic specificity identical to mAD cAZ. Administering a TNF-inhibiting amount of an anti-TNF chimeric antibody which has epitopic specificity identical to mAD cAZ. Administering activity identical to mAD cAZ. Is useful cortreating cachexia in humans, particularly a cachexia associated with cancer, HIV or ALDS. This is the amino acid sequence of mouse cAZ light chain variable region used in the creation of TNF alpha-antibody fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; tumour necrosis factor-alpha; TNF-alpha; A2; cA2; complementarity determining region; bacterial infection; viral infection; fungal infection; parasitic infection; inflammatory disease; sarcoidosis; atherosclerosis; autoimmune disease; rheumatord arthritis; systemic lupus erythematosus; neurodegenerative disease; Huntington's Chorea; Parkinson's disease; malignancy; lymphoma; carcinoma; alcohol-induced hepatitis; light chain variable region;
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                                                                                                                                                                                                                                                    Length 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody light chain variable region polypeptide.
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                                                                                                                                                                                                                                                  100.0%; Score 557; DB 6;
100.0%; Pred. No. 8.6e-38;
iive 0; Mismatches 0;
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92US-00853606.
92US-00943852.
93US-00010406.
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94US-00192093.
94US-00192102.
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94US-00324799.
95US-00570674.
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2001US-00756398
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                                                                                                                                                                                                                                                                       Local Similarity 100.
                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2003144484-A1.
                                                                                                                                                                                                                       Sequence 107 AA;
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04-FEB-1994
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04-FEB-1994
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Matches
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The invention relates to a human anti-tumour necrosis factor (TNF)
antibody or its antigen binding fragment that competitively inhibits
binding of antibodies A2 or cA2 to human TNF-alpha. The invention also
relates to a composition comprision the antibody or its antigen binding
fragment and a carrier, a human light or heavy chain that specifically
binds human TNF-alpha and competitively inhibits binding of A2 or cA2 to
binds human TNF-alpha, the human light or heavy chain consisting of the
complementarity determining regions of the light or heavy chain of A2 or
CA2, and a human light or heavy chain framework region and an isolated
nucleic acid that encodes the above human heavy or light chain. The
antibody is useful in in vivo diagnosis and therapy of TNF-alpha-mediated
antibody is useful in in vivo diagnosis and therapy of TNF-alpha-mediated
carcinogies and conditions, such as infections (e.g. bacterial, viral,
atherosclerosis), autoimmune diseases (e.g. rheumatoid arthritis,
systemic lugus erythmatosus), neurodegenerative diseases (e.g. lymphomas,
carcinomas) and alcohol-induced hepatitis. This sequence represents the
consec cA2 antibody light chain variable region polypeptide.
                                                                          New human anti-tumor necrosis factor (TNF) antibody or its antigen binding fragment that competitively inhibits binding of A2 or cA2 to human TNF-alpha, useful for diagnosing and treating TNF-alpha-mediated
                                                                                                                                                                                                                    Disclosure; SEQ ID NO 3; 97pp; English.
                                                                                                                                                             diseases, e.g. infection.
WPI; 2003-744929/70.
N-PSDB; ADC46569.
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Sequence 107 AA;

1 DILLTQSPAILSVSPGERVSFSCRASQFVGSSIHWYQQRTNGSPRLLIKYASESMSGIPS 60 1 DILLIQSPAILSVSPGERVSFSCRASQFVGSSIHWYQQRINGSPRLLIKYASESMSGIPS 60 0; Gaps Query Match
100.0%; Score 557; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 8.6e-38;
Matches 107; Conservative 0; Mismatches 0; Indels ( 61 RFSGSGSGTDFTLSINTVESEDIADYYCQQSHSWPFTFGSGTNLEVK 107 61 RFSGSGSGTDFTLSINIVESEDIADYYCQQSHSWPFTFGSGTNLEVK 107 qq à

Search completed: December 15, 2004, 17:16:37 Job time : 109.053 secs

Sequence 62, Appl Sequence 62, Appl Sequence 62, Appl Sequence 63, Appl Sequence 83, Appl Sequence 83, Appl Sequence 83, Appl Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 11, Appli Sequence 11, Appli Sequence 14, Appli Sequence 14, Appli

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GENERAL INFORMATION:
APPLICANT: Le, Junming
APPLICANT: Vilcek, Jan
APPLICANT: Vilcek, Jan
APPLICANT: Obadona, Peter E.
APPLICANT: Ghrayeb, John
APPLICANT: Knight, David M.
APPLICANT: Siegel, Scott A.
TITLE OF INVENTION: ANTI-TNF ANTIBODIES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & David C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA

ZIP: MASIBAGENESCUS
ZIP: 02173

COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATOMIN PC-DOS/MS-DOS
SOFTWARE: PATOMIN ROPE: US/08/192,102
FILING DATE: 04-FEB-1994
CLASSIFICATION NUMBER: US/08/192,093
FILING DATE: 04-FEB-1994
APPLICATION NUMBER: US/08/192,093
FILING DATE: 02-FEB-1994
APPLICATION NUMBER: US/08/193,093
FILING DATE: 29-JAN-1993
PRICH APPLICATION NUMBER: US/08/193,413
FILING DATE: 10-FEB-1993
PRICH APPLICATION NUMBER: US/08/193,852
FILING DATE: 11-FEP-1992
PRICH APPLICATION NUMBER: US/08/193,852
FILING DATE: 11-FEP-1992
PRICH APPLICATION NUMBER: US/07/670,827
FILING DATE: 18-MRR-1992
PRICH APPLICATION NUMBER: US/07/670,827
FILING DATE: 18-MRR-1991
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US-07-634-278-62
US-08-477-728-62
US-08-487-200-62
US-08-484-537-62
US-07-634-278-83
US-07-634-278-83
US-08-474-040-83
US-08-474-040-83
US-08-477-200-83
US-08-484-557-83
US-08-485-246-6
US-08-485-246-6
US-08-47-352-1
US-09-247-352-4
US-09-247-352-4
US-09-247-352-4
                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
US-08-192-102-3
; Sequence 3, Application US/08192102
; Patent No. 5656272
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CITY: Lexington
STATE: Massachusetts
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Sequence 8, A
Sequence 20,
Sequence 4, A
Sequence 1, A
                                                                                                                                                       December 15, 2004, 17:10:19; Search time 27.4602 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, 1
Sequence 4, 1
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                                                                                                                                                                                                                                       US-09-897-724-3
557
1 DILLTQSPAILSVSPGERVS.......CQQSHSWPFTFGSGINLEVK 107
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Sequence 3,
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'cgnz_6/ptodata1/iaa/5A_COMB.pep:*
'cgnz_6/ptodata1/iaa/5B_COMB.pep:*
'cgnz_6/ptodata1/iaa/6A_COMB.pep:*
'cgnz_6/ptodata1/iaa/6A_COMB.pep:*
'cgnz_6/ptodata1/iaa/8E_COMB.pep:*
'cgnz_6/ptodata1/iaa/PCTUS_COMB.pep:*
'cgnz_6/ptodata1/iaa/PCTUS_COMB.pep:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-324-799-3

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US-09-133-119-3

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US-09-133-119-3

US-09-244-38-1

US-09-244-3

US-09-244-38-1

US-09-245-399-4

US-09-245-399-4

US-08-420-4

US-08-476-399-4

US-08-476-399-4

US-08-476-399-4

US-08-476-176B-4

US-08-476-176B-4

US-08-476-176B-4

US-08-476-176B-4

US-08-476-176B-4

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US-08-476-18-8

US-08-476-18-8

US-08-476-18-8

US-08-65-59-8

US-08-65-59-8

US-08-65-59-8

US-08-65-59-8

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US-08-476-176-8

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US-08-476-18-8

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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US 07/853,606
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-192-861A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Knight, David M.
APPLICANT: Siegel, Scott A.
TITLE OF INVENTION: ANTI-TAN ANTIBODIES AND PEPTIDES
TITLE OF INVENTION: OF HUMAN TUMOR NECROSIS FACTOR
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTE: V21/3
COMPUTE: D21/3
COMPUTE: FLODPY disk
COMPUTE: TEM PC compatible
COMPUTE: TEM PC-DOS(WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,799
FILING DATE: 04-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,102
FILING DATE: 04-FEB-1994
PRIOR APPLICATION NUMBER: US 08/192,861
FILING DATE: 04-FEB-1994
PRIOR APPLICATION NUMBER: US 08/192,413
FILING DATE: 02-FEB-1993
PRIOR APPLICATION NUMBER: US 08/191,413
FILING DATE: 2-FEB-1993
PRIOR APPLICATION NUMBER: US 08/191,406
FILING DATE: 2-JAN-1993
PRIOR APPLICATION NUMBER: US 08/191,406
FILING DATE: 1-SEP-1992
FRIOR APPLICATION NUMBER: US 07/943,852
FILING DATE: 1-SEP-1992
REFERENCE/DOCKET NUMBER: NYU93-01M3
| TELECOMMUNICATION INPERMATION:
| TELEPHONE: (617) 861-6240
| TELEPHONE: (617) 861-9540
| TELEPA: (617) 861-9540
| INFORMATION FOR SEQ ID NO: 3:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 107 amino acids |
| TYPE: amino acid |
| TYPE: amino acid |
| TOPOLOGY: linear |
| MOLECULE TYPE: protein |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08324799 Patent No. 5698195
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Vilcek, Jan
Daddona, Peter E.
Ghrayeb, John
                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 107; Conservative
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CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Le, Junn
APPLICANT: vilcek,
APPLICANT: Daddona,
APPLICANT: Ghrayeb,
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US-08-324-799-3
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Sequence 3, Application US/08192861A

Patent No. 5919452

GENERAL INFORMATION:

APPLICANT: Le, Junming

APPLICANT: Le, Junming

APPLICANT: Daddona, Peter E.

APPLICANT: Ghrayeb, John

APPLICANT: Siegel, Scott A.

TITLE OF INVENTION: METHODS OF TREATING TNF'-MEDIATED DISEASE USING

TITLE OF INVENTION: CHIMERIC ANTI-TNF ANTIBODIES (As Amended)

NUMBER OF SEQUENCES:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DILLIQSPAILSVSPGERVSFSCRASQFVGSSIHWYQQRTNGSPRLLIKYASESMSGIPS 60
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100.0%; Score 557; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.2e-46;
Matches 107; Conservative 0; Mismatches 0; Indels
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UNIVERSAL APPLICATION DATA:
APPLICATION NUMBER:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
BRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
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FILING DATE:
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BRIOR APPLICATION DATA:
APPLICATION NUMBER:
BRIOR AP
                                                                                                                                    FILING DATE: 18-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: BEOOK, DAVIG E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: 01593-01M4
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 861-6240
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/670,827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acids
TOPOLOGY: lin
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1 DILLTQSPAILSVSPGERVSFSCRASQFVGSSIHWYQQRTNGSPRLLIKYASESMSGIPS 60
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| Sequence 3, Application US/08192093A
| Sequence 3, Application US/08192093A
| Patent No. 6284471
| GENERAL INFORMATION:
| APPLICANT: Le, Junming
| APPLICANT: Ghraybe, John
| APPLICANT: Ghraybe, John
| APPLICANT: Knight, David M.
| APPLICANT: Knight, David M.
| APPLICANT: Knight, David M.
| TITLE OF INVENTION: ANTI-TNF' ANTIBODIES AND ASSAYS EMPLOYING
| TITLE OF INVENTION: ANTI-TNF' ANTIBODIES
| VUMBER OF SEQUENCES: 19
| CORRESPONDER EN ADDRESS:
| STREET: Two Militia, Drive STREET: Two Militia, Drive STREET: Two Militia, Drive COUNTRY: USA
| COUNTRY: USA Compatible
| COMPUTER READABLE FORM: MEDIUM TYPE: IMP RC Compatible
| COMPUTER: IMP RC Compatible
| COMPUTER: IMP RC Compatible
| COMPUTER: PatentIn Release #1.0, Version #1.25
| CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTDFTLSINTVESEDIADYYCQOSHSWPFTFGSGTNLEVK 107
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100.0%; Score 557; DB 3;
Best Local Similarity 100.0%; Pred. No. 6.2e-46;
Matches 107; Conservative 0; Mismatches 0;
             PRIOR APPLICATION NUMBER: 08/192,861
FILING DATE: 04-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/013,413
FILING DATE: 02-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010,406
FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,852
FILING DATE: 11-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,852
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/670,827
FILING DATE: 18-MAR-1992
PRIOR APPLICATION NUMBER: US 07/670,827
FILING DATE: 18-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: BEOOK, DAVIG E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: 22,592
REFERENCE/DOCKET NUMBER: NYU93-01M4P
TELEFONNE: (617) 861-6240
TELEFAX: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22,592
ER: NYU93-01M4A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 107 amino acids
amino acid
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US-08-192-093A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 557; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.2e-46;
Matches 107; Conservative 0; Mismatches 0; Indels C
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APPLICANT: Le, Junming
APPLICANT: Le, Junming
APPLICANT: Daddona, Peter E.
APPLICANT: Girayeb, John
APPLICANT: Siegel, Scott A.
ITILE OF INVENTION: ANTI-TNF ANTIBODIES AND PEPTIDES
ITILE OF INVENTION: OF HUMAN TUMOR NECROSIS FACTOR
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds. P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACTOR FACTOR Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/133,119 FILING DATE:
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
PELICATION NUMBER: US 07/670,827
FILING DATE: 18-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: BEFORE 22,592
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: NYU93-01M2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (781) 861-6240
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/570,674
FILING DATE: 11-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/324,799
FILING DATE: 18-CCT-1994
PRIOR APPLICATION NUMBER: 08/122,093
FILING DATE: 04-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIE: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JMBER: 08/192,102
04-FEB-1994
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FILING DATE: 04-FEB-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09133119
Patent No. 6277969
                                                                                                                                                                                                                                                                                                                                     : 107 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
FILING DATE: 04-FE
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US-09-133-119-3
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1 DILLIQSPAILSVSPGERVSFSCRASQFVGSSIHWYQQRTNGSPRLLIKYASESMSGIPS 60
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                        PRIOR PILING DATE: 1993-01-29
PRIOR PILING DATE: 1993-01-29
PRIOR PILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1992-09-11
PRIOR FILING DATE: 1992-09-11
PRIOR FILING DATE: 1992-09-11
PRIOR FILING DATE: 1992-09-12
PRIOR FILING DATE: 1992-03-13
PRIOR FILING DATE: 1992-03-13
PRIOR FILING DATE: 1992-03-14
PRIOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 557; DB 4; Length 107; Best Local Similarity 100.0%; Pred. No. 6.2e-46; Matches 107; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTDFTLSINTVESEDIADYYCQQSHSWPFTFGSGTNLEVK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIJDENSS, JOSHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCES: 42
CORRESPONDENCES: 42
CORRESPONDENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: FLODEY disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/232,081B
FILING BATE:
CLASSIFICATION: ANAMATON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.8%; Score 506;
APPLICATION NUMBER: U.S. 08/010,406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INPORMATION:
NAME: SYENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 40: SEQUENCE CHARACTERISTICS: TENGTH: 107 amit
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MOLECULE TYPE: protein
US-08-232-081B-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-756-301B-3
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US-08-232-081B-40
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APPLICANT: Le Junming
APPLICANT: Vilcek, Jan
APPLICANT: Vilcek, Jan
APPLICANT: Deldona, Peter
APPLICANT: Might, Jan
APPLICANT: Staght, John
APPLICANT: Staght, David M.
APPLICANT: Stagel, Scott
TITLE OF INVENTION: Human Tumor Necrosis Factor
FILE OF INVENTION: Human Tumor Necrosis Factor
FILE REFERENCE: 0975,1005-008
CURRENT APPLICATION NUMBER: US/09/756,301B
FRIOR FILING DATE: 1998-08-12
PRIOR FILING DATE: 1998-08-12
PRIOR FILING DATE: 1998-08-12
PRIOR FILING DATE: 1994-10-18
PRIOR FILING DATE: 1994-10-18
PRIOR FILING DATE: 1994-02-04
                                        FILING DATE: U4-FEB-15.7

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/013,413

FILING DATE: 02-FEB-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010,406

FILING DATE: 29-JAN-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0/943,852

FILING DATE: 11-SEP-1992

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 0/853,606

FILING DATE: 18-MAR-1991
APPLICATION NUMBER: US 0/670,827

FILING DATE: 18-MAR-1991

ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 22,592

REGERENCE/DOCKET NUMBER: NYU93-01M3

TELEPHONE: (617) 861-6240

TELEPHONE: (617) 861-6240

TELEPHONE: (617) 861-6240

TELEPHONE: (617) 861-6240

SEQUENCE CHARACTERISTICS:
TENETH. 107 amino acids
APPLICATION NUMBER: US/08/192,093A
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Patent No. 6790444
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amino acid
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Best Local Similarity 100.
Matches 107; Conservative
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US-09-756-301B-3
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                                                                        1 DILLIQSPAILSVSPGERVSFSCRASQFVGSSIHWYQQRINGSPRLLIKYASESMSGIPS
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                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/07956399;
Patent No. 5876717
GENERAL INFORMATION:
APPLICANT: SHIMMATION:
APPLICANT: TAKI, SHINSUKE
APPLICANT: TAKI, SHINSUKE
APPLICANT: TAKI, SHINSUKE
TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF BINDING TO HEAVY
TITLE OF INVENTION: CHAINS OF IL-2 RECEPTORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSER: P.C.
                                                                                                                                                                                                  195 RFSGSGSGTDFTLSINSVESEDIADYYCQHTNSWPTTFGGGTKLEIK 241
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                                                                                                                                                                        61 RFSGSGSGTDFTLSINTVESEDIADYYCQQSHSWPFTFGSGTNLEVK 107
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88.8%; Pred. No. 3.9e-40;
live 7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/956,399
FILING DATE: 19921005
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5876717man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-586-0
TELEPOWNICATION INFORMATION:
TELEPOWNICATION INFORMATION:
TELEPOWNICATION INFORMATION:
TELEPOWNICATION INFORMATION:
     88.8%; Pred. No. 2.6e-40;
tive 7; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : (703) 413-3000
(703) 413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 239 amino acids
AMINO ACID
     Best Local Similarity 88.8 Matches 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1755 S. CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 95; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-956-399-2
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APPLICANT: Barbera-Guillem, Emilio
APPLICANT: Barbera-Guillem, Emilio
APPLICANT: Barbera-Guillem, Emilio
FILE ROFENSWE: Phy-03
CURRENT APPLICATION NUMBER: US/09/940,391
CURRENT APPLICATION NUMBER: 09/244,369
PRIOR APPLICATION NUMBER: 09/244,369
PRIOR APPLICATION NUMBER: 00/077,970
PRIOR APPLICATION NUMBER: 60/077,970
PRIOR PILING DATE: 1999-02-06
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Barbera-Guillem, Emilio
TITLE OF INVENTION: Method for detecting and surgically removing lymphoid tissue invo
TITLE OF INVENTION: Lumor progression
TITLE OF INVENTION: tumor progression
CURRENT PELING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: US 60/073,882
PRIOR APPLICATION NUMBER: US 60/073,882
PRIOR APPLICATION NUMBER: US 60/077,970
PRIOR FILING DATE: 1998-03-13
NUMBER: OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 DILLIQSPAILSVSPGERVSFSCRASQNIGTSIHWYQQRTNGSPRLLIKYASESVSGIPS 194
                                                                        1 DILLIQSPAILSVSPGERVSFSCRASQFVGSSIHWYQQRINGSPRLLIKYASESMSGIPS 60
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                                                                                                       1 DILLIQSPAILSVSPGERVSFSCRASQTIGTSIHWYQRRTNGSPRLLIKYASBSISGIPS
                            0; Gaps
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                                                                                                                                                                        61 RESGSGSGTDFTLSINTVESEDIADYYCQQSHSWPFTFGSGTNLEVK 107
                                                                                                                                                                                                                    61 RFSGSGSGTDFTLSINSVESEDIADYYCQQSSSWPLTFGAGTKLELK 107
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88.8%; Pred. No. 2.6e-40;
tive 7; Mismatches 5; Indels
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                            4; Indels
     89.7%; Pred. No. 4.4e-41; tive 7; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09244369B Patent No. 6418338 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-940-391-1; Sequence 1, Application US/09940391; Patent No. 6760612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 88.8
Matches 95; Conservative
                         96; Conservative
Best Local Similarity
Matches 96; Conserv
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; ORGANISM: Mus sp.
US-09-940-391-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Mus sp. US-09-244-369B-1
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                                                                                                                                                                                                                                                                                                                    US-09-244-369B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA.
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-SEPTEMBER-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 106 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IXPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-326-362-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-08-476-176B-4
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Patent No. 5730981
GENERAL INFORMATION:
APPLICANT: Besslet, Klaus
APPLICANT: Seeman, Gerhard
APPLICANT: Dippold, Wolfgang
TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,
TITLE OF SEQUENCES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DILLIQSPAILSVSPGERVSFSCRASQFVGSSIHWYQQRINGSPRLLIKYASESMSGIPS
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GENERAL INFORMATION:
APPLICANT: SHIMMANNA, TOSHIRO
APPLICANT: ALMANNA, TOSHIRO
APPLICANT: ALXI, SHINGUKE
APPLICANT: TAKI, SHINGUKE
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: CHAINS OF IL-2 RECEPTORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: ALINGLON
STATE: Virginia
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,399
FILING DATE: 19921005
CLASSIFTATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 587617man F.
RECISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-586-0
TELEPHONE: (703) 413-3200
TELEPHONE: (703) 413-3200
TELEPHONE: (703) 413-3200
TELEPHONE: (703) 413-3200
TELEPHONE: CASO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein US-07-956-399-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM
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ZIP: 20005-3315
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STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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1 DIQLIQSPAILSVSPGERVSFSCWASQSIGTSIHWYQQRINGSPRLLIKYSSESISGIPS 60
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APPLICANT: Hardman, No. 5958708man
APPLICANT: Saldama, Jose
APPLICANT: Saldama, Jose
TITLE OF INVENTION: Sessaped monoclonal antibodies against an
TITLE OF INVENTION: immunoglobulin isotype
TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5958708artis Patent Department
STREET: 59 Route 10
CITY: East Hanover
STRIE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/476,176B
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OPERATING SYSTEM: PC-DUS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/326,362
FILING DATE:
FLING DATE:
PRICK APPLICATION: 435
PRICK APPLICATION NUMBER: US 08/032,863
APPLICATION NUMBER: US 08/032,863
APPLICATION NUMBER: DE P42 08 795.3
ATTORNEY/AGENT INFORMATION:
NAME: ESTANDIA, CONTRACTOR NUMBER: 22,220
REGISTRATION NUMBER: 32,220
REGISTRATION NUMBER: 32,220
REGISTRATION NUMBER: 32,220
REGISTRATION NUMBER: 02481-1276-00000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION
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61 RFSGSGSGTEFTLNINSVESEDIADYYCQQSDSWPTTFGGGTKLBIK 107
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Score 494; DB 3; Length 107;
Pred. No. 6e-40;
9; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: No. 6072035artis Patent Department STREET: 59 Route 10 CITY: Bast Hanover STATE: New Jersey COUNTRY: USA ZIP: 07936-1080 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/W8-DOS SOFTWARE: PECHTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/485,246A
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Best Local Similarity 86.9%; Pred. No. 6e-40;
Matches 93; Conservative 9; Mismatches
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CLASSIFICATION: 424

PRIOR APPLICATION: 424

PRIOR PAPLICATION DATA:

APPLICATION NUMBER: 08/127,721

FILING DATE: 27-SEPTEMBER-1993

APPLICATION NUMBER: US 07/952,802

FILING DATE: 25-SEPTEMBER-1992

ATTORNEY AGENT INFORMATION:

REGISTARION NUMBER: 33,200

REFERENCE/DOCKET NUMBER: 4.19276/A/P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 277-5110

TELEPHONE: (908) 277-5110
          88.7%;
86.9%;
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          Query Match
Best Local Similarity 86.94
Matches 93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08127721A
| Sequence 4, Application US/08127721A
| Patent No. 6066718
| GENERAL INFORMATION:
| APPLICANT: Hardman, No. 6066718man
| APPLICANT: Saldanha, Jose
| TITLE OF INVENTION: Reshaped monoclonal antibodies against an TITLE OF INVENTION: Remanaged monoclonal antibodies against an TITLE OF INVENTION: Remanaged monoclonal antibodies against an TITLE OF INVENTION: Remanaged monoclonal antibodies against an TITLE OF INVENTION: Abanaged monoclonal antibodies against an TITLE OF INVENTION: SADURESS:
| NUMBER OF SEQUENCES: 55
| ADDRESSEE: No. 6066718artis Patent and Trademark Department STREET: 59 Route 10
| CITY: Bast Hanover STRATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGTDFTLSINTVESEDIADYYCQQSHSWPFTFGSGTNLEVK 107
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                                                                                                                                                                                                                                                                                                                                                                                              88.7%; Score 494; DB 2; Length 107; 86.9%; Pred. No. 6e-40; tive 9; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZTATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08127,721A
FILING DATE: 27-SEPTEMBER-1993
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6066718ak, Henry P.
REGISTRATION NUMBER: 33.200
REGISTRATION NUMBER: 33.200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPRONE: (908) 277-4316
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                          4-19276/A/P2/CIP
                                NAME: No. 5958708ak, Henry P.
REGISTRATION VMBER: 33,200
REGISTRATION VMBER: 4-1927
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRA: (908) 277-5110
TELEPRA: (908) 277-4306
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 107 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 86.9
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-127-721A-4
                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-476-176B-4
                                                                                                                                                                                                                                                                                                    linear
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                                                  DILLIQSPAILSVSPGERVSFSCRASQFVGSSIHWYQQRINGSPRLLIKYASESMSGIPS
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  Gaps
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                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08485246A
Patent No. 6072035
GENERAL INFORMATION:
APPLICANT: Hardman, No. 6072035man
APPLICANT: Kolbinger, Frank
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an TITLE OF INVENTION: immunoglobulin isotype
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
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Search completed: December 15, 2004, 17:22:50 Job time : 28.4602 secs

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us-09-897-724-3.rapb

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1 DILLTQSPAILSVSPGERVS......CQQSHSWPFTFGSGTNLEVK 107
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

				Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli
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SUMMAKIES			Description	Sequence 3,	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Sequence	Sequence	Sequence
			ID	US-09-756-301A-3	US-09-927-703-3	US-09-766-535A-3	US-09-756-161A-3	US-09-756-398B-3	US-09-897-724-3	US-10-010-229-3	US-10-043-450-3	US-10-044-534-3	US-10-043-432-3	US-10-208-145-3	US-10-198-845-3	US-10-227-488-3
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			Match Length DB	107	107	107	107	107	107	107	107	107	107	107	107	107
	dю	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
			Score	557	557	557	557	557	557	557	557	557	557	557	557	557
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Sequence 3, Appli Sequence 31, Appli Sequence 31, Appli Sequence 31, Appli Sequence 42, Appli Sequence 23, Appli Sequence 24, Appli Sequence 27, Appli Sequence 28, Appli Sequence 28, Appli Sequence 129, Appli Sequence 129, Appli Sequence 129, Appli Sequence 129, Appli Sequence 48, Appli	
14 557 100.0 107 14 US-10-187-121-3 15 557 100.0 107 14 US-10-176-460-3 17 557 100.0 107 14 US-10-176-460-3 18 557 100.0 107 14 US-10-200-795-3 20 557 100.0 107 14 US-10-371-443-3 21 557 100.0 107 14 US-10-371-443-3 22 557 100.0 107 14 US-10-371-443-3 23 557 100.0 107 14 US-10-379-866-3 24 557 100.0 107 14 US-10-379-866-3 25 557 100.0 107 14 US-10-379-866-3 26 557 100.0 107 14 US-10-379-866-3 27 557 100.0 107 16 US-10-379-866-3 28 557 100.0 107 16 US-10-65-971-3 29 557 100.0 226 15 US-10-411-026-42 29 557 100.0 226 15 US-10-411-026-42 29 557 100.0 226 15 US-10-411-039-42 30 557 100.0 226 15 US-10-411-039-42 31 557 100.0 226 16 US-10-410-997-42 32 557 100.0 226 16 US-10-310-9 35 557 100.0 226 16 US-10-310-9 36 557 100.0 226 16 US-10-310-9 37 502 90.1 107 15 US-10-318-129 38 502 90.1 107 15 US-10-318-210-9 41 502 90.1 244 1 US-10-239-656-49 44 502 90.1 50 15 US-10-239-656-49 45 502 90.1 107 15 US-10-239-656-49 46 502 90.1 500 15 US-10-239-656-49 47 502 90.1 500 15 US-10-239-656-49	RESULT 1  US-09-756-301A-3  Sequence 3, Application US/09756301A  PAPLICANT: Le, Junming  APPLICANT: Le, Junming  APPLICANT: Le, Junming  APPLICANT: Might, David M.  APPLICANT: Ghrayeb, John  APPLICANT: Ghrayeb, John  APPLICANT: Might, David M.  APPLICANT: Ghrayeb, John  APPLICANT: 1998-09-10-10-10-10-10-10-10-10-10-10-10-10-10-

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Matches
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                                                                                                                                                                                                                                                                                                            Length 107;
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APPLICANT: Knight, David M.
APPLICANT: Siegel, Scott
TITLE OF INVENTION: Human Tumor Necrosis Factor
TITLE OF INVENTION: Human Tumor Necrosis Factor
TITLE OF INVENTION: Human Tumor Necrosis Factor
FILE REFERENCE: 0975.1005-013
CURRENT APPLICATION NUMBER: U.S. 09/756,398
PRIOR FILING DATE: 2001-08
PRIOR FILING DATE: 1998-08-12
PRIOR FILING DATE: 1998-08-12
PRIOR PILING DATE: 1998-08-12
PRIOR FILING DATE: 1994-10-18
PRIOR PILING DATE: 1994-10-18
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1992-03-18
PRIOR FILING DATE: 1992-03-18
PRIOR FILING DATE: 1992-03-18
PRIOR FILING DATE: 1992-03-18
PRIOR FILING DATE: 1991-03-18
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PRIOR APPLICATION NUMBER: U.S.07/670,827
PRIOR FILING DATE: 1991-03-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 107
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Patent No. US20020022720A1
GENERAL INFORMATION:
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APPLICANT: Vilcek, Jan
APPLICANT: Daddona, Peter
APPLICANT: Ghrayeb, John
                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-756-301A-3
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ORGANISM: Mus Balb/c
US-09-927-703-3
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Best Local Similarity
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SEQ ID NO 3
LENGTH: 107
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                                                      1 DILLIQSPAILSVSPGERVSFSCRASQFVGSSIHWYQQRTNGSPRLLIKYASESMSGIPS
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llarity 100.0%; Pred. No. 9.2e-45;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ghrayeb, John
APPLICANT: Knight, David M.
APPLICANT: Siegel, Scott
TITLE OF INVENTION: Anti-TNF Antibodies and Pept
TITLE OF INVENTION: Human Tumor Necrosis Factor
FILE REFERENCE: 0975.1005.010
CURRENT APPLICATION NUMBER: US/09/766,535A
CURRENT FILING DATE: 2001.01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: U.S. 09/133,119
PRIOR PILING DATE: 1998-08-12
PRIOR PILING DATE: 1998-08-12
PRIOR PELING DATE: 1995-12-11
PRIOR PELING DATE: 1994-01-018
PRIOR PILING DATE: 1994-02-04
PRIOR PELING DATE: 1993-01-29
PRIOR PELING DATE: 1993-01-29
PRIOR APPLICATION NUMBER: U.S. 08/103,413
PRIOR PILING DATE: 1993-01-29
PRIOR APPLICATION NUMBER: U.S. 09/013,413
PRIOR PILING DATE: 1993-02-02
PRIOR APPLICATION NUMBER: U.S. 07/943,652
PRIOR PELING DATE: 1992-09-11
PRIOR PILING DATE: 1992-09-11
PRIOR PILING DATE: 1992-03-18
PRIOR PILING DATE: 1991-03-18
PRIOR PILING DATE: 1991-03-18
     Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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US-09-756-161A-3
; Sequence 3, Application US/09756161A
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     107; Conservative
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APPLICANT: Vilcek, Jan
APPLICANT: Daddona; Peter
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Best Local Similarity
Matches 107; Conserva
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US-09-766-535A-3
                                                                                                                                                                                                                                                                                                                               -09-766-535A-3
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1 DILLIQSPAILSVSPGERVSFSCRASQFVGSSIHWYQQRTNGSPRLLIKYASESMSGIPS 60
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US-097/24-34

US-097/24-34

Publication No. US20030175837A1

GENERAL INFORMATION:

APPLICANT: Le, Junming

APPLICANT: Daddona, Peter

APPLICANT: Baddona, Peter

APPLICANT: Siegal, Scott

TITLE OF INVENTION: Human Tumor Necrosis Factor

FILE REFERENCE: 0975-1005-007

TITLE OF INVENTION: Human Tumor Necrosis Factor

FILE REFERENCE: 0975-1005-007

FILE REPERENCE: 0975-1005-007

FILE REPERENCE: 1091-02-04

PRIOR PILICATION NUMBER: U.S. 08/192,093

PRIOR PILING DATE: 1993-01-29

PRIOR PILING DATE: 1993-01-29

PRIOR PILING DATE: 1993-01-29

PRIOR PILING DATE: 1993-02-02

PRIOR PILING DATE: 1992-09-11

PRIOR FILING DATE: 1992-09-11
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100.0%; Score 557; DB 10;
Best Local Similarity 100.0%; Pred. No. 9.2e-45;
Matches 107; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 1998-08-12
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PRIOR FILING DATE: 1995-12-11
PRIOR FILING DATE: 1995-12-11
PRIOR FILING DATE: 1994-10-18
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1993-02-04
PRIOR FILING DATE: 1993-02-04
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-02
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PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1992-09-11
PRIOR FILING DATE: 1991-03-18
NUMBER OF SEQ ID NOS: 19
SEQ ID NOS: 19
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; ORGANISM: Mus Balb/c
US-09-756-398B-3
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PUblication No. US20030017584A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Vilcek, Jan
APPLICANT: Daddona, Peter
APPLICANT: Grayeb, John
APPLICANT: Knight, David M.
APPLICANT: Knight, David M.
APPLICANT: Siegel, Scott
ITILE OF INVENTION: Anti-TNY Antibodies and Peptides of
ITILE REFERENCE: 0975.1005-006
ITILE REFERENCE: 0975.1005-006
CURRENT FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: US/09/756,398B
PRIOR APPLICATION NUMBER: US. 09/133,119
                                                                                                                                                APPLICANT: Ghrayeb, John
APPLICANT: Ghrayeb, John
APPLICANT: Knight, David M.
APPLICANT: Siegel, Scott
TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
TITLE OF INVENTION: Anti-TNF Antibodies and Peptides
CURRENT FILING DATE: 2001-01-08
PRIOR PILING DATE: 1994-01-018
PRIOR PILING DATE: 1994-02-04
PRIOR APPLICATION NUMBER: U.S. 08/192,093
PRIOR PILING DATE: 1994-02-04
PRIOR PILING DATE: 1993-01-29
PRIOR PILING DATE: 1993-01-29
PRIOR PILING DATE: 1993-01-29
PRIOR PILING DATE: 1993-02-02
PRIOR PILING DATE: 1993-02-02
PRIOR PILING DATE: 1992-03-18
PRIOR PILING DATE: 1993-03-18
PRIOR PILING DATE: 1993-03-18
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Best Local Similarity 100.0%; Pred. No. 9
Matches 107; Conservative 0; Mismatches
                . US20020132307A1
VFORMATION:
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; ORGANISM: Mus Balb/c
US-09-756-161A-3
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APPLICANT: Le, Junming
APPLICANT: Vilcek, Jan
APPLICANT: Ordedown Peter
APPLICANT: Grayeb, John
APPLICANT: Grayeb, John
APPLICANT: Siegel, Scott
TILE OF INVENTION: Anti-TNP Antibodies and Peptides of
TILE OF INVENTION: Human Tumor Necrosis Factor
FILE REPERENCE: 0975.1065.013
CURRENT APPLICATION NUMBER: US/09/927,703
FRICA PAPLICATION NUMBER: US/09/927,703
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 19 Windows Version 4.0
SEQ ID NO 3
LENGTH: 107
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Publication No. US20020141996A1
GENERAL INFORMATION:
APPLICANT: Le, Junming
APPLICANT: Le, Junming
APPLICANT: Daddona, Peter
APPLICANT: Grayeb, John
APPLICANT: Siegel, Scott
APPLICANT: Siegel, Scott
TITLE OF INVENTION: Human Tumor Necrosis Factor
FILLE REPERENCE: 0975.1005-013
FILLE REPERENCE: 0975.1005-013
CURRENT APPLICATION NUMBER: US/10/043,450
CURRENT FILING DATE: 2002-01-10
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                                                                                                          100.0%; Score 557; DB 10; 100.0%; Pred. No. 9.2e-45;
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Best Local Similarity 100."
Matches 107; Conservative
                                                                                                        Query Match
Best Local Similarity 100.
Matches 107; Conservative
                       ; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-897-724-3
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LENGTH: 107
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| FRICE FILES DATE: 2010.01
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APPLICANT: Le, Junning
APPLICANT: Ullcek, Jan
APPLICANT: Glarabeb, John
APPLICANT: Grayeb, John
APPLICANT: Grayeb, John
APPLICANT: Grayeb, John
APPLICANT: Grayeb, John
APPLICANT: Siegel, Scott Thus Tumor Necrosis Factor
TITLE OF INVENTION: Human Tumor Necrosis Factor
FILE REFERENCE: 0975.1005.006
CURRENT APPLICANTON NUMBER: US/09/756,398
PRIOR PILING DATE: 1202-07-29
PRIOR PELING DATE: 1208-08-12
PRIOR PILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: U.S. 08/70,674
PRIOR APPLICATION NUMBER: U.S. 08/192,067
PRIOR PILING DATE: 1994-02-04
PRIOR PILING DATE: 1993-01-29
PRIOR PILING DATE: 1993-01-20
PRIOR PILING DATE: 1993-01-10
PRIOR PILING DATE: 1993-01-10
PRIOR PILING DATE: 1993-01-10
PRIOR PILI
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100.0%; Pred. No. 9.2e-45;
tive 0; Mismatches 0;
    PRIOR APPLICATION NUMBER: U.S. 07/943,852
PRIOR FILING DATE: 1992-09-11
PRIOR APPLICATION NUMBER: U.S. 07/853,606
PRIOR FILING DATE: 1992-03-16
PRIOR PLING DATE: 1991-03-18
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 3
SEQ ID NO 3
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Best Local Similarity 100.0
Matches 107; Conservative
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ORGANISM: Mus Balb/c
US-10-043-432-3
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; Sequence 3, Application US/10043432
; Publication No. USC030054004A1
GENERAL INFORMATION:
APPLICANT: Le, Junming
APPLICANT: Vileck, Jan
APPLICANT: Use, Junming
APPLICANT: Siegel, Scott
TITLE OF INVENTION: Arti-TUF Antibodies and Peptides of
TITLE OF INVENTION: Arti-TUF Antibodies and Peptides of
TITLE OF INVENTION: Human Tumor Necrosis Factor
CURRENT FILING DATE: 2001-01-0
PRIOR PELICATION NUMBER: U.S. 09/133,119
PRIOR PELICATION NUMBER: U.S. 08/192,093
PRIOR PELICATION NUMBER: U.S. 08/102,093
PRIOR PELICATION NUMBER: U.S. 08/102,403
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100.0%; Score 557; DB 13;
Best Local Similarity 100.0%; Pred. No. 9.2e-45;
Matches 107; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: U.S. 08/192,102
PRIOR FILING DATE: 1994-02-04
PRIOR PILING DATE: 1994-02-04
PRIOR PILING DATE: 1994-02-04
PRIOR PILING DATE: 1994-02-04
PRIOR PLING DATE: 1994-02-04
PRIOR PLING DATE: 1994-02-04
PRIOR PLING DATE: 1994-02-04
PRIOR PLING DATE: 1993-01-29
PRIOR PLING DATE: 1993-01-29
PRIOR PLING DATE: 1993-01-29
PRIOR PLING DATE: 1993-02-02
PRIOR PLING DATE: 1993-02-02
PRIOR PLING DATE: 1993-02-03
PRIOR PLING DATE: 1993-03-11
PRIOR PLING DATE: 1992-09-11
PRIOR PLING DATE: 1992-03-18
PRIOR PLING DATE: 1992-03-18
PRIOR PLING DATE: 1992-03-18
PRIOR PLING DATE: 1992-03-18
PRIOR PLING DATE: 1991-03-18
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; ORGANISM: Mus Balb/c
US-10-044-534-3
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US-10-198-498-3

Sequence 3, Application US/10198045

Publication No. US200301444841

GENERAL INFORMATION:

APPLICANT: Le, Junming

APPLICANT: Lo, Junming

APPLICANT: Grayeb, John

APPLICANT: Siegel, Socie

APPLICANT: Siegel, Socie

APPLICANT: Siegel, Socie

TITLE OF INVENTION: Anti-ITPF Antibodies and Peptides of

PRIOR FILING DATE: 1994-00-0-0-18

PRIOR FILING DATE: 1995-12-11

PRIOR FILING DATE: 1994-02-04

PRIOR FILING DATE: 1993-01-29

PRIOR PRIOR FILING DATE: 1993-01-29

PRIOR FILING DATE: 1993-01-29

PRIOR PRIOR FILING DATE: 1993-01-20-4
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                                Indels
Best Local Similarity 100.0%; Pred. No. 9.2e-45; Matches 107; Conservative 0; Mismatches 0;
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US-10-227-488-3
; Sequence 3, Application US/10227488
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; ORGANISM: Mus Balb/c
US-10-198-845-3
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   PRIOR FILING DATE: 1994-02-04
PRIOR APPLICATION NUMBER: U.S. 08/192,093
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1993-01-03
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PRIOR FILING DATE: 1993-01-29
PRIOR PLING DATE: 1993-02-02
PRIOR PLING DATE: 1993-02-02
PRIOR PLING DATE: 1992-02-11
PRIOR PLING DATE: 1992-02-18
PRIOR PLING DATE: 1992-03-18
PRIOR PLING DATE: 1992-03-18
PRIOR APPLICATION NUMBER: U.S. 07/670,827
PRIOR PRIOR DATE: 1991-03-18
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Job time : 93.3761 secs
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US-10-176-460-3
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APPLICANT: Let, Jumming
APPLICANT: Daddona, Peter
APPLICANT: Daddona, Denn
APPLICANT: Ghrayeb, John
APPLICANT: Siegel, Scott
APPLICANT: Siegel, Scott
TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
TITLE OF INVENTION: Human Tumor Necrosis Factor
FILER REPRENCE: 0975-1005-006
CURRENT APPLICATION NUMBER: US/10/176,460
CURRENT APPLICATION NUMBER: US/09/756,398
PRIOR APPLICATION NUMBER: U.S. 09/133,119
PRIOR PILING DATE: 1998-08-12
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: U.S. 08/570,674
PRIOR FILING DATE: 1994-10-18
PRIOR APPLICATION NUMBER: U.S. 08/192,102
PRIOR FILING DATE: 1994-10-18
PRIOR PILING DATE: 1994-02-04
PRIOR PILING DATE: 1994-02-04
PRIOR FILING DATE: 1994-02-04
PRIOR PILING DATE: 1994-02-04
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100.0%; Score 557; DB 14;
Best Local Similarity 100.0%; Pred. No. 9.2e-45;
Matches 107; Conservative 0; Mismatches 0;
CURRENT FILING DATE: 2002-06-28

PRIOR APPLICATION NUMBER: US 09/756,398

PRIOR FILING DATE: 2001-01-08

PRIOR PILING DATE: 1998-08-12

PRIOR PILING DATE: 1994-02-04

PRIOR PLING DATE: 1993-01-29

PRIOR PLING DATE: 1993-01-29

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PRIOR PLING DATE: 1992-09-11

PRIOR PLING DATE: 1992-09-11
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ORGANISM: Mus Balb/c
US-10-187-121-3
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December 15, 2004, 17:09:55; Search time 22.2522 Seconds (without alignments) 462.659 Million cell updates/sec
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557
1 DILLTQSPAILSVSPGERVS.......CQQSHSWPFTFGSGTNLEVK 107
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G44151 B49047 X3HU41 JE0243 S57444 B26555 B26555 B306331 B3060331 KVMS43 S40337 C30608 B30608	ALIG	- mouse) revision 03-Nc.es, A.R. 88 anti-DNA and iD:88315787;	ny vegion; pi ny vegion; immuno immunoglobulin in homology <imm> '5%; Score 504;</imm>	Pred.   9, Mis	/SFSCRASQ          /SFSCRASQ	SEDVADY	region - huma  region - huma  revision 30-  , H.; Diamant  chimerization  fulb:93138402;  n v region; im  n v region; im  n v region; im  remunoglobulin  remu
0040000000H0000		14) - mouse mouse co-revisi Rees, A. 1988 of anti-MUID:883	N '	% %	SER'S	-:- NSV	region  rection  H.;  Chim  JID:9
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6 6 6 66 66 66 66 66 66 66 66 66 66 66		a chain es: Mus 03-Nov- 03-Nov- 03-Nov- 01-141 i. V regi i. V regi sion: C3 sion: C3 called the cal	referen family: rds: het /Domain: Match	al Si 94;	1 1 19 0— 1 19 0— 18	61 R	a chain a chain a chain a Sion: Wow sion: PN sio
ਸ਼		RESULT 1 C30502 IG kappa chain V region (D444) IG Species: Mus musculus (house r C,Date: 03-Nov-1988 #sequence_rr C,Accession: C30502 R,Eilat, D.; Webster, D.M.; Reei J. Immunol. 141, 1745-1753, 1988 A,Title: V region sequences of A,Reference number: A30502; MUII A,Accession: C30502 A,Status: preliminary A,Molecule type: mRNA A,Residues: 1-108 *RIL>	A; Cross C; Super; C; Keywol F; 16-90,	Best Loc Matches	\$ B \$	ପ୍ର	RESULT 2 PN0445 C) Specipes chain precursor c) Specipes: Howe sapiens (c) Date: 30.56p-1993 #sequence c) Date: 30.56p-1993 #sequence c) Date: 30.52p-1993 #sequence c) Date: 30.52p-1992 C) Aritle: A general method A) Reference number: PN044 A) Reference number: PN044 A) Reference number: PN044 A) Reference number: B1992 A) Residues: 1-128 *KAL> A) Cross-references: GB:LOC; Superfamily: immunoglob C; Superfamily: immunoglob C; Superfamily: immunoglob C; Reywords: heterotetrame F; 1-10/Domain: signal sequence control of the contraction of the

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F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining
F;98-106/Region: framework 4
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C; Species: Mus musculus (house mouse)
C; Species: Musculus (house mouse)
R; Pech, M.; Hochtl, J.; Schnell, H.; Zachau, H.G.
Nature 291, 668-670, 1981
A; Title: Differences between germ-line and rearranged immunoglobulin V-kappa coding sequences to the mouse of the musculus (house)
A; Reference number: A93259; MUID: 81220975; PMID: 6264318
A; Residues: 1-115 <-PBC>
A; Molecule type: DNA
A; Residues: Bredicted <-PBC
C; Superfamily: immunoglobulin heterotetramer subunit consists of two identical light (kap C; Superfamily: immunoglobulin homology cimal sequence #status predicted <-PBC
C; Superfamily: immunoglobulin homology <-PBC
C; Superfamily: immunoglobulin homology <-PBC
C; Superfamili: immunoglobulin homology <-PBC
F; 1-115 / Product: Iq kappa chain V region (L7) #status predicted <-MAT>
F; 43-108 / Disulfide bonds: #status predicted <-PBC
C; Molecule type: DNA
A; #status pr
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PLO267
IG kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession PLO267
C;Accession: DLO267
C;Accession: DLO267
C;Accession: DLO267
C;Accession: DLO27
C;Access
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                                                                                                                                                                                  1 DILLTQSPAILSVSPGERVSFSCRASQFVGSSIHWYQQRTNGSPRLLIKYASESMSGIPS
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 93.7%; Pred. No. 1.1e-34;
Matches 89; Conservative 5; Mismatches 1; Indels
         Length 128;
                                                                                              5; Indels
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    Score 497; DB 2;
Pred. No. 3.3e-37;
9; Mismatches 5;
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    89.2%;
                                                                                              Conservative
                                                   Similarity
                                                                                    93;
    Query Match
Best Local
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CySpecies: Mus musculus (house mouse)
CySpecies: Mus musculus (house mouse)
CySpecies: Mus musculus (house mouse)
CyDate: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
CyAccession: 833479
RyTakeda, Y.; Wise, K.S.; Hoffman, R.W.
Nucleic Acids Res. 20, 4039, 1392
AyTitle: Nuclectide sequences of immunoglobulin heavy and light chain V-regions from a mAxReference number: 835479; MUID:92375706; PMID:1387203
AyAccession: 835479
AyAccession: Sisty
AyACce
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#status predicted <MAT>
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       Length 106;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-12/Domain: signal sequence (fragment) #status predicted <SIC
F;13-123/Product: Iq kappa chain V region (fragment) #status prr
F;28-102/Domain: immunoglobulin homology <IMM>
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       DB 2;
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77.9%; Score 434; DB 2; 74.5%; Pred. No. 1e-31; ive 17; Mismatches 1
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RESULT 9
H1082
Ig light chain V region (clone 165.54) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C; Accession: PH1082
A; Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B A; Reference number: PH1081
A; Reference number: PH1082
A; Accession: PH1082
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-87 - TIL>
A; Residues: 1-87 - TIL>
A; Residues: 1-87 - TIL>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain precursor V region (MAK33) - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999 C;Accession: A26471 R;Buckel, P:,Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K. A;Buckel, P:, 13-19, 1987 A;Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a A;Reference number: A91572; MUID:87248058; PMID:3110009
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C;Species: Mus musculus (house mouse)
C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B43413
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosidues: 1-138 GBUC>
A;Cross-references: GB:M16162; NID:g196893; PIDN:AAA38823.1; PID:g196894
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin bomology
F;Pyvords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <NAT>
F;21-138/Product: Ig kappa chain V region #status predicted <MAT>
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  RFSGSGSGTDFTLTINSVETEDFGMYFCQQTNSWPHTFGGGTKLEIK 107
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72.0%; Pred. No. 2.3e-30;
iive 18; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.7%; Score 421.5; DB 2
larity 92.0%; Pred. No. 1.1e-30;
Conservative 5; Mismatches 1
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Best Local Similarity 72.0°
Matches 77; Conservative
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Best Local Similarity
Matches 81; Conserv
  61
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C, Species: Mus musculus (house mouse)
C, Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C, Accession: A45722
R, Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu. J. Virol. 67, 489-496, 1993
A, Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu A, Reference number: A45722, MUID: 93100833; PMID: 7677958
A, Accession: A45722
A, Abocession: A45722
A, Motocession: A45722
A, Motoce sextracted from NCBI backbone (NCBIP:120589)
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: glycoprotein
F, 16-90/Domain: immunoglobulin homology < IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B45722
R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu A;Reference number: A45722; MUID:93100833; PMID:7677958
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                                                                                                               13 DIVLTQSPATLSVTPGDKVSLSCRASQSISNYLHWYQQKSHESPRLLIKYVSQSISGIPS
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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Residues: 1-107 «SIM»
A;Note: sequence extracted from NCBI backbone (NCBIP:120590)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: glycoprotein
F;16-90/Domain: immunoglobulin homology <IMM>
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                             Indels
Pred. No. 4e-31;
7; Mismatches 12;
Similarity 72.9%; Pr 78; Conservative 17;
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R;Tomiyama, Y:; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; Kurf Biol. Chem. 267, 18085-18092, 1992

J. Biol. Chem. 267, 18085-18092, 1992

A;Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific A;Reference number: A43413; MUID:92388177; PMID:151741

A;Reference number: A43413; MUID:92388177; PMID:1517241

A;Recession: B43413

A;Recession: preliminary; not compared with conceptual translation

A;Recidens: 1-104 < TON>

A;Recession: memorglobulin vergion; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;13-87/Domain: immunoglobulin homology < INM>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 326346
R;Stark, S.E.; Caton, A.J.
T. Exp. Med. 174, 613-624, 1991
A;Tele: Antibodies that are specific for a single amino acid interchange in a protein A;Reference number: 226346
A;Accession: 226346
A;Accession: 226346
A;Accession: preliminary
A;Accession: preliminary
A;Accession: 226346
A;Accession: preliminary
C;Superfamily: mmnnoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-88/Domain: immunoglobulin homology <IMM>
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$19975
Ig kappa chain V region (M-T408) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Decies: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: $19975
R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
Submitted to the EMBL Data Library, March 1992
A;Bescription: Structural characterization of CD4 mAb.
A;Reference number: $19963
A;Accession: $19975
A;Accession: $19975
A;Accession: $19375
A;Relatus: preliminary
A;Relatus: preliminary
A;Residues: 1103 <WEI>
A;Residues: 1103 <WEI>
A;Cross-references: EMBL:X65097; NID:g52296; PIDN:CAA46225.1; PID:g52297
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                                                                                                                                                                                                                                                                                                                                                                                Length 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                74.1%; Score 413; DB 2; 72.1%; Pred. No. 7.2e-30; tive 18; Mismatches 11;
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Best Local Similarity 72.18
Best Tocal Similarity 72.18
The 75, Conservative
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Ly Adapta diant precipion (Man)

C) Species: Homo sapiens (Man)

C) Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C) Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

R) Siberstein, L.E.; Litwin, S.; Carmack, C.E.

R) Siberstein, L.E.; Litwin, S.; Carmack, C.E.

J. Exp. Med. 169, 1631-1643, 1899

A, Title: Relationship of variable region genes expressed by a human B cell lymphoma secr.

A, Reference number: PLO106; MUID:89235583; PMID:2541221

A, Accession: PLO106

A, Molecule Lype: mRNA

A, Molecule Lype: mRNA

A, Residues: 1-144 «SIL.

A, Residues: 1-144 «SIL.

C) Superfamily: immunoglobulin V region; immunoglobulin homology

C) Superfamily: immunoglobulin homology «IMM»

F; 1-20/Domain: signal sequence #status predicted «SIG»

F; 20-110/Domain: W region «VRE»

F; 30-110/Domain: complementarity-determining 1

F; 70-76/Region: complementarity-determining 3

F; 10-76/Region: complementarity-determining 3

F; 118-127/Domain: C region (fragment) «CRE»
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C; Accession: S09963
R; Reininger, L; Shibata, T; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A; Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie.
A; Reference number: S09955; MUID: 90269328; PMID: 2347362
A; Rocession: S09963
A; Residues: 1-111 < REI>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;11-85/Domain: immunoglobulin homology <IMM>
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C,Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hercotetramer, immunoglobulin
F;16-94/Domain: immunoglobulin homology <IVM>
                                                                                                                                             Query Match 69.7%; Score 388; DB 2; Length 10
Best Local Similarity 67.6%; Pred. No. 1.2e-27;
Matches 69; Conservative 17; Mismatches 16; Indels
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64.5%; Pred. No. 1.8e-25;
tive 15; Mismatches 23;
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Best Local Similarity 65.5%; Pred. No. 1.7e-25;
Matches 74; Conservative 12; Mismatches 19; Indels 8; Gaps 3;
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Search completed: December 15, 2004, 17:21:47 Job time: 23.2522 secs

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ALIGNMENTS
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02478 MOUSE

072473 MOUSE

KV30 MOUSE

KV30 MUSE

KV3M HUMAN

KV3M HUMAN

KV3L HUMAN

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QGY17 homo sapien
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1 DILLTQSPAILSVSPGERVS.......CQQSHSWPFTFGSGTNLEVK 107
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RN [1]

RP SEQUENCE FROM N.A.

RA MEDILINES-120375; PubMed=6264318;

RA MEDILINES-12120375; PubMed=6264318;

RA Pech M., Hochtl J., Schnell H., Zachau H.G.;

RT "Differences between germ-line and rearranged immunoglobulin V kappa RT coding sequences suggest a localized mutation mechanism.";

RL "Differences between germ-line and rearranged immunoglobulin V kappa RT coding sequences suggest a localized mutation mechanism.";

RL "Differences between germ-line and rearranged immunoglobulin V kappa RT ST CC at the 3' end of the intron. The alternate would code for a protein lacking residues 17-19.

RP PDIS JULY X-ray; L=21-115.

DR PDB; JULY X-ray; L=21-115.

JULY X-ray; L=21-11
RESULT 1

KV51 MOUSE STANDARD; PRT; 115 AA.

AC P01642;
DT 21-UUL-1986 (Rel. 01, Created)
DT 21-UUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE IG kappa chain V-V region L7 precursor (Fragment).

B IG kappa chain V-V region L7 precursor (Fragment).

C Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

DX NOEL TaxID=10090;
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Framework-3.
Complementarity-determining-3.
By similarity.
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KV1M HUMAN

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Best Local Similarity
Matches 71; Conserv
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                                                                                                                   1 DILLTOSPAILSVSPGERVSFSCRASOFVGSSIHWYQQRTNGSPRLLIKYASESMSGIPS
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                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TRAIN-Be.Slei, TISSUB-Spleen,
Liang Z., Xie C., Chen C., Kreeka D., Hsu K., Zhou J.X., Mohan C.;
"Antinuclear autoantibodies from Be.Slei mice.";
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                        Score 468; DB 1; Length 115;
Pred. No. 2e-40;
5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 SGSGSGTDFTLSINTVESEDIADYYCQQSHSWPFTFGSGTNLEVK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Indels
                                                     C17BEC758C577E00 CRC64;
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
ANA immunoglobulin kappa light chain (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                        02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
ANA immunoglobulin kappa light chain (Fragment).
                                                                                                                                                                        81 RFSGSGGTDFTLSINSVESEDIADYYCQQSNSWP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.5%; Score 404; DB 2; 69.5%; Pred. No. 7.8e-34; iive 18; Mismatches 14;
                                                                                                                                                           61 RFSGSGSGTDFTLSINTVESEDIADYYCQQSHSWP 95
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89
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ilarity 93.7%;
Conservative
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Best Local Similarity 69.54
Matches 73; Conservative
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115 AA;
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les 89; Conserv
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AAR10984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TPATLSVTPGDSVSLSCRASQSISNNLHWYQQKSHESPRLLIKYASQSISGIPSRFSGSG
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STRAIN=B6.Sle1; TISSUE=Spleen;
STRAIN=B6.Sle1; TISSUE=Spleen;
STRAIN=B6.Sle1; TISSUE=Spleen;
Strain Stra
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STRAIN=B6.Sle1; TISSUE-Spleen;
Straing Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
"Antinuclear autoantibodies from B6.Sle1 mice.";
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY436890; AAR11050.1; -.
NON TER
1 1 105
SEQUENCE 105 AA, 11377 MW; 9698895429461258 CRC64;
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
ANA immunoglobulin kappa light chain (Fragment).
Mus musculus (Mouse).
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AAR11029; 02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
ANA immunoglobulin (sappa light chain (Fragment).
Mus musculus (Mouse).
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Best Local Similarity 70.1%
Matches 68; Conservative
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                                                                                            Gaps
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Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
ANA immunoglobulin kappa light chain (Fragment).
ANA immunoglobulin kappa light chain (Fragment).
Eukaryota; Metazoa; Chordaea; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae
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STRAIN=B6.Sle1; TISSUE=Spleen;
Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan
"Antinuclear autoantibodies from B6.Sle1 mice.";
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY436875; AAR11035.1; -.
                                                                 Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 65.5%; Score 365; DB 2; Length 96; I Similarity 69.5%; Pred. No. 7e-30; 66; Conservative 16; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=B6.Sle1; TISSUE=Spleen;
Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., I
"Antinuclar autoantibodies from B6.Sle1 mice.";
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY436877; AAR11037.1; -.
                                                                Query Match
66.4%; Score 370; DB 2; Length 10
Best Local Similarity 69.3%; Pred. No. 2.3e-30;
Matches 70; Conservative 14; Mismatches 17; Indels
                        103 AA; 11064 MW; C3D2C4D1B230F426 CRC64;
                                                                                                                                                                         61 RESGSGSGTDFTLSINTVESEDIADYYCOOSHSWPFTFGSG 101
                                                                                                                                                                                                  RFSGSGSGTDFTLSINGVETEDFGMYFCQQIDSWPYTSEGG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 96 AA; 10432 MW; 6E2F60254DBD5515 CRC64;
                                                                                                                                                                                                                                                                                 AAR11037;

2-MAR-2004 (TrEMBLrel. 27, Created)

02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 SGSGSGTDFTLSINTVESEDIADYYCQQSHSWPFT 97
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EMBL; AY436869; AAR11029.1;
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                                                                                                                                                                                                                                                                     PRELIMINARY;
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AAR11035;
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Matches
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                                                                                                                                                             Gaps
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STRAIN=B6.Sle1; TISSUE=Spleen;
Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
Submitted (SEP-2003 to the EMBL/GenBank/DDBJ databases.

EMBL, AX436847; AAR11007.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                         Length 105;
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SEQUENCE FROM N.A.
Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X.,
Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X.,
"Antrinuclear autoantibodies from B6.Slel mice.";
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AV436866; AAR1026.1; -
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103 AA; 11029 MW; 0D7AB0DE9983992B CRC64;
                                                   OBDE221254B167F7 CRC64;
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                      65.5%; Score 365; DB 2; L
69.5%; Pred. No. 7.7e-30;
tive 16; Mismatches 13;
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
ANA immunoglobulin kappa light chain (Fragment).
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AARI1026.
02-MAR-2004 (TYEMBLrel. 27, Created)
02-MAR-2004 (TYEMBLrel. 27, Last sequence update)
02-MAR-2004 (TYEMBLrel. 27, Last annotation update)
ANA immunoglobulin kappa light chain (Fragment)
Mus musculus (Mouse)
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105 AA; 11298 MW;
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Best Local Similarity 67.00
The 69, Conservative
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KV3F HUMAN
P01624;
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RISSUE=22386257; PubbWed=12477932;

RIAUSDER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Antschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Antschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toonlyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wishin T.B., Toonlyuki S., Carninci P., Prange C.,

Raha S.S., McEwan P.J., McKernan K.J., Males V.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

And M.H., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Ryminski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

C. Mones S.J., Marra M.A.,

T. "Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                            ; Score 361; DB 2; Length 95;
; Pred. No. 1.8e-29;
16; Mismatches 13; Indels
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC030813; AAH30813.1; -.
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234 AA; 25530 MW; 6316E8DEF8D132F8 CRC64;
  95
10329 MW; FF70654DBD551510 CRC64;
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Last sequence update)
Last annotation update)
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ad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                SGSGSGSDFTLSINSVEPEDVGVYYCONGHSFPPT 95
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                                                                64.8%;
                                                                                       69.5%;
                                                                                                            Conservative
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95
95 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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Midper D.G., Capra J.D.;

The amino acid sequence of the variable regions of the light chains

The amino acid sequence of the variable regions of the light chains

I from two idiotypically cross reactive 1gM anti-gamma globulins.";

L. Ann. Immunol. (Paris) 127C:261-271(1976).

C. - MISCELLANEOUS: This chain was isolated from an 1gM with anti-gamma globulin activity.

C. - MISCELLANEOUS: This chain was isolated from an 1gM with anti-gamma globulin activity.

DR GLOSST6, Cextracellular; NAS.

GO, GO:0003823; F:antigen binding; NAS.

GO, GO:0003823; F:antigen binding; NAS.

GO, GO:0005956; P:immune response; NAS.

GO, GO:0005956; P:immune response; NAS.

DR Ffam; PF0047; Ig; 1.

BROSTE; PR0041110; Ig-1ike.

BROSTE; PSSO835; IG_LIKE; 1.

BROSTE; PSSO835; IG_LIKE; 1.

ETT. DISCURTED

ETT. DI
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NOSI_TaxID=9606;
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MEDLINE-98277139; PubMed=9614934;
Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ۲.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.0%; Score 356.5; DB 1; Length 62.0%; Pred. No. 6.1e-29; ive 21; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11922 MW; 62821DDC6A8ABA86 CRC64;
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EMBL; AF035031; AAD56267.1; -.
PIR; B30609; B30609.
                                                                                                                                       21-JUL-1986 (Rel. 01, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) IG kappa chain V-III region POM.
Ä.
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109
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PRT;
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                                                                                          (Rel. 01, Created)
(Rel. 01, Last sequ
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67; Conservative
STANDARD;
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Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A blatchenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,

A blatchenko L., Marusha K., Parmer A.A., Rubin G.M., Hong L.,

Stapleton M., Saares M.B., Donaldo M.F., Casavant T.L., Scheez T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robak S.A., McEwan P.J., McKerran K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

W. Hilaton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                 Zhou J.X., Mohan C.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=B6.Sle1; TISSUE=Spleen;
Liang Z., Xie C., Chen C., Kreska.D., Hsu K., Zhou J.X.,
"Antinuclear autoantibodies from B6.Sle1 mice.";
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY436887; AAR11047.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 AA; 10636 MW; 6850A3AB53C66D39 CRC64;
                                O2-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
ANA immunoglobulin kappa light chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Best Local Similarity bs...
Best 67; Conservative
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                                                                                                                                                             Mus musculus (Mouse).
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TISSUE=Spleen;
Strausberg R.;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0AR-2004 (TrEMBLrel. 25, Last annotation update)
Anti-VIPase light chain variable region (Fragment).
Nus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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STRAINBALBYC TISSUE-Hyperimmunized spleen;
Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF316284; AAM64202.1; -.
PIR; A33933; A33933.
PIR; A31933; A31933.
INTERPROSE; PLOSE.
HSSP; PO1837, 25CB.
InterPro; IPR00310; Ig-like.
InterPro; IPR00356; Ig-v.
SMART; SM00406; IGY; 1.
SMART; SM00406; IGY; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 SRFSGSGSGTDFTLSINTVESEDIADYYCQQSHSWPFTFGSGTNLEVK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGTDFTLSINTVESEDIADYYCQQSHSWPFTFGSGTNLEVK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RFSGSGGTEFTLISSLQFEDFAVYYCQHYNNWPFTFGPGTKVDIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 108;
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                                                                                                                                                                                                                                                                                                                                                                              108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      63.9%; Score 356; DB 2;
60.7%; Pred. No. 6.8e-29;
ive 21; Mismatches 21;
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PIR; C30609; C30609.
PIR; D30609; D30609.
PIR; S34099; S34099.
HSSP; P01625; ILVE.
INCERPIO: IPRO07110; Ig-like.
INCERPIO: IPRO07110; Ig-like.
Fam; PP00047; ig; I.
PROSITE; PS50835; IG_LIKE; I.
NON TER I 108 108
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nes 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65, Conservative
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114 AA;
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AAR11047

RESULT 14 AAR11047 ID AAR11

Query Match

Best Loc Matches

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Search completed: December 15, 2004, 17:20:53 Job time : 119.836 secs
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Query Match 62.6%; Score 348.5; DB 2; Length 235; Best Local Similarity 61.1%; Pred. No. 9.8e-28; Matches 66; Conservative 20; Mismatches 21; Indels 1; Gaps

E Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

R InterPro; IPR003599; Ig.

InterPro; IPR007110; Ig-like.

R InterPro; IPR003599; Ig-d.

R InterPro; IPR003599; Ig-d.

R InterPro; IPR003596; Ig-WHC.

R InterPro; IPR003596; Ig-WHC.

R Pfam; PF0047; ig; 2.

R SMART; SM00409; IG-2.

R SMART; SM00409; IG-2.

R SMART; SM00409; IG-2.

R PROSITE; PS0299; IG-MHC; UNKNOWN\_1.

R PROSITE; PS0290; IG-MHC; UNKNOWN\_1.

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Human tra Anti-TNFa Anti-TNFa Remicade

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An anti-TNF chimeric antibody may be administered for treating TNF-alpha mediated Crohn's disease in a human. The anti-TNF chimeric antibody competitively inhibits binding of TNF to monoclonal antibody cA2. The anti-TNF antibody does not bind to one or more epitopes in amino acids 11-13, 37-42, 49-57 or 155-157 of hTNF, but does bind to one or more epitopes included in amino acids between 87-108 or both 87-108 and 59-80 of hTNF. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treatment of Crohn's disease - by administering humanised cA2 antibody specific for tumour necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        necrosis factor; Crohn's disease; cA2 antibody.
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ADF89618
ADH89385
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ADL29707
ADL70772
AMR55861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW28532 standard; protein; 119 AA
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92US-00943852.
93US-00010406.
93US-00013413.
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(first entry)
 WPI; 1997-414547/38.
N-PSDB; AATB7442.
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361.932 Million cell updates/sec
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1 EVKLEESGGGLVQPGGSMKL.....RNYYGSTYDYWGQGTTLTVS
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Compugen Ltd.
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                  GenCore version (c) 1993 - 2004
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Maximum Match 100%
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Sequence 119 AA;
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                                                                                                                                     HYAESVKGRFTISRDDSKSAVYLQMTDLRTEDTGVYYCSRNYYGSTYDYWGQGTTLTVS 119
                                                                                                                                                         Tumour necrosis factor; human; hTNF; rheumatoid arthritis; malignancy; anti-TNF chimeric antibody; inhibitor; therapy; diagnosis; infection; chronic inflammatory disease; autoimmune disease; heavy chain; neurodegenerative disease; variable region.
                                                                                                  EVKLEESGGGLVQPGGSMKLSCVASGFIFSNHWMWVRQSPEKGLEWVAEIRSKSINSAT
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tumour necrosis factor.
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                         100.0%; Score 636; DB 2;
100.0%; Pred. No. 1.3e-49;
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                                                    0; Mismatches
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UNIV NEW YORK MEDICAL CENT.
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92US-00853606.
93US-0001406.
93US-00013413.
94US-00192093.
94US-00192102.
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invention for alleviating symptoms or pathologies involving TNF, such as bacterial, viral or parasitic infections, chronic inflammatory diseases, autoimmune diseases, malignancies and/or neurodegenerative diseases
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18s 119; Conservative
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N-PSDB; AAX81706.
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chimeric antibodies are useful for treating and/or diagnosing TNF-alpha mediated diseases such as immune and autoimmune pathologies e.g. rheumatoid arthritis and especially systemic lupus expthematosus (SLE), thyroidosis, graft versus host disease, scleroderma, diabetes mellitus, and Graves' disease, inflammatory diseases (other than septic shock), neurodegenerative disorders, cerebellar cortical degenerations, multiple systems degenerations (e.g. Mencel, Dejerine-Thomas, Sh-Drager, and Machado-Joseph, Refsum's disease, abetalipoprotemia, ataxia, telangiectasia, mitcohondrial multi-system disorder, amyotrophic lateral sclerosis, infantile and juvenile spinal muscular atrophy, Alzheimer's disease, Down's Syndrome im middle age, Diffuse Lewy body disease, Demetria of Lewy body type, Wernicke-Koraakoff syndrome, chronic alcoholism, Creutzfeldt-Jakob disease, sub-acute sclerolising panencephalitis, Hallerrorden-Spatz disease, dementia pugilistica, lumphomas, other TNF-secreting tumors or alcohol-induced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, tumour necrosis factor-alpha, TNF-alpha, chimeric antibody, immunoglobulin, inflammation; cancer; cachexia; sepsis; endotoxic shock; infection; chronic inflammatory disease, auto-immune disease, malignancy; neurodegenerative disease; crohn's disease, rheumatoid archritis; A2; vascular endothelial growth factor; VEGF, VEGF-mediated disease.
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                                                                                                                                                                                                                                                                                                    100.0%; Score 636; DB 2; 100.0%; Pred. No. 1.3e-49;
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92US-00853606.
93US-0001406.
93US-00013413.
94US-00192102.
94US-00192861.
94US-00324779.
94US-00324779.
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(first entry)
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Matches 119, Conservative
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                                                                                                                                                                                                                                                                       Sequence 119 AA;
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Chimeric.
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29-JAN-1993;
02-FEB-1993;
04-FEB-1994;
04-FEB-1994;
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11-DEC-1995
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The present sequence represents the heavy chain variable region of a chimeric human-murine A2 antibody (GA2) which binds to epitopes of human cumour necrosis factor (TNP)-alpha. Chimeric antibodises of the invention comprise at least part of a human immunoglobulin constant region and at least part of a human immunoglobulin variable region. The chimeric antibodies are useful in vivo diagnosis and therapy of TNF-alpha-mediated pathologies and conditions. They can also neutralize human TNF-alpha-mediated pathologies and conditions. This is useful as TNF is known to be under physiological conditions. This is useful as TNF is known to be involved in e.g. pro-inflammatory actions, wasting associated with cancer and other diseases (cachexia), gram-negative sepsis and endotoxic shock. Antibodies can be used to treat and/or diagnose bacterial, parasitic or viral infections, chronic inflammatory diseases, auto-immune diseases, malignancies and neurodegenerative diseases (such as Crohn's disease and rheumatoid arthritis). As inhibition or antagonism of TNF also decreases the expression of vascular endothelial growth factor (VEGF), the antibodies are also useful to treat VEGF-mediated diseases. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                             New chimeric antibody binding an epitope specific for human tumor necrosis factor alpha useful in treatment and diagnosis of tumor necrosis factor alpha related conditions e.g. Crohn's disease.
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Siegel
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Knight D,
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100.0%; Pred. No. 1.3e-49
ive 0; Mismatches 0
Ghrayeb J,
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                                                                                                                                                                          English
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Vilcek J, Daddona P,
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92US-00943852.
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Best Local Similarity 100.
Matches 119; Conservative
                                                                                                                                                                          16B; 93pp;
                                       2001-615872/71.
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                                                                                                                                                                      Claim 40; Fig
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18-MAR-1992;
11-SEP-1992;
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  Le J,
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ID AAE1
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                                                                                                                                                                                                                                                        The invention relates to chimeric anti-tumour necrosis factor (TNF) antibodies. These chimeric antibodies comprises two light chains and two heavy chains, each of the chains comprising at least part of a human for munoglobulin (Ig) constant region and at least part of a non-human of variable region, where the antibodies are capable of binding an epitope specific for human TNF-alpha. Anti-TNF antibodies or peptides may be used in research, therapeutic and diagnostic methods, specifically for diagnostic antibody. TNF-relating animals or human having pathologies or conditions associated with the presence of a substance reactive with an anti-TNF antibody. TNF-related pathologies include acute and chronic immune and autoinmune disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis), infections (e.g. systemic lupus erythematosus, rheumatoid arthritis), infections (e.g. bacterial, viral, fungal or parasitic infections), inflammatory diseases (e.g. uncrative colitis, chorea or semile chorea, disorders of the basal ganglia or cerebellar disorders), malignant pathologies (e.g. leukaemia, lymphomas), or alcoholinduced hepatitis. The anti-TNF peptide or antibodies may also be used for immunoassays, which detect or quantitate TNF or anti-TNF antibodies.

The present sequence is mouse heavy chain variable region of chimeric A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; tumour necrosis factor; TNF; anti-TNF antibody; cA2; infection; sepsis; cachexia; acquired immunodeficiency syndrome; AIDS; septic shock; chronic inflammatory disease; disseminated intravascular coagulation; atherosclerosis; ulcerative colitis; chronic inflammatory bowel disease; autoimmune disease; rheumatoid arthritis; diabetes mellitus; graft versus host disease; drave's disease; alcohol-induced hepatitis; demyelinating disease; active disease; multiple sclerosis; demyelinating disease; acute transverse myelitis; vascular endothelial growth factor-mediated disease;
                                                                                                                                                                 Chimeric anti-tumor necrosis factor (TNF) antibodies useful for diagnosing or treating TNF-associated pathologies or conditions, e.g. chronic and acute immune, autoimmune disorders, and microbial infections.
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                                                                                         Siegel SA;
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                                                                                         Knight D,
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                                                                                         Ghrayeb J,
                                          (UYNY-) UNIV NEW YORK MEDICAL CENT. (CENZ.) CENTOCOR INC.
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              93US-00013413.
                                                                                          Dadonna P,
93US-00010406
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Best Local Similarity 100.
Matches 119; Conservative
                                                                                                                      WPI; 2001-595467/67.
N-PSDB; AAD18193.
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                                                                                       Vilcek J,
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29-JAN-1993;
              02-FEB-1993;
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The present sequence represents the cloned heavy chain variable region of antibody cA2, which is directed against tumour necrosis factor (TNF). The specification describes anti-TNF antibodies, such as cA2. The anti-TNF antibody is useful for alleviating symptoms or pathologies involving TNF, such as bacterial, viral or parasitic infections (e.g. sepsis, cachexia, acquired immunodeficiency syndrome (AIDS) and septic shock), chronic inflammatory diseases (disseminated intravascular coagulation, atherosclerosis, ulcerative colitis and chronic inflammatory bowel diseases, autoimmune diseases (e.g. rheumatoid antihritis, diabetes mellitus, graft versus host disease and Grave's diseases), alcohol-induced hepatitis, malignancies and/or neurodegenerative diseases (e.g. multiple acclerosis, demyelhating diseases and acute transverse myelitis). The anti-TNF antibody is also useful in the treatment of vascular endothelial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid molecule encoding heavy or light chain variable regions of anti-tumor necrosis factor antibody, useful for alleviating symptoms or pathologies involving tumor necrosis factor.
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100.0%; Pred. No. 1.3e-49;
.ive 0; Mismatches 0; Indels
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                                                                                                                                 91US-00670827.
92US-00854606.
92US-00943852.
93US-0010406.
93US-00102093.
94US-00192102.
94US-00192102.
94US-00192102.
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US6277969-B1.
                                                                                        12-AUG-1998;
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Matches
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ID ABG;
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AC ABG;
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DT 28-1
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us-09-897-724-5.rag

18-MAR-1991 Le J, Mus 

anti-TNF peptide; neurodegenerative disease; multiple sclerosis; acquired immunodeficiency syndrome; AIDS; demyelinating disease; acquired immunodeficiency syndrome; AIDS; demyelinating disease; acute transverse myelitis; extrapyramidal disorder; lesion; cerebellar disorder; basal ganglia disorder; Huntington's cholera; movement disorder; senile cholera; Parkinson's disease; spinal ataxia; syngressive supranuclaar palsy; spinocerbellar degeneration; systemic disorder; neurogenic muscular atrophy; Down's Syndrome; amyotrophic lateral sclerosis; Alzheimer's disease; chronic alcoholism; of cetuzfeldt-Jakob disease; Hallervorden-Spatz disease; neurobrotective; antiparkinsonian; human TNPalpha; hTNPalpha; mutine; mouse; cA2, chimeric A2; heavy chain variable region; mutant; antihuman TNP IgG1 antibody; IgG1 kappa; mutein. Human-murine chimeric anti-hTNFalpha cA2 heavy chain variable region. anti-TNF antibody; TNFalpha; necrosis factor-alpha; US2002106372-A1. Homo sapiens, 08-AUG-2002 Mus sp. Synthetic. Chimeric.

18-JAN-2001; 2001US-00766535

91US-00670827. 92US-0085366. 92US-0091365. 93US-0010406. 93US-0013413. 94US-00192102. 94US-00192861. 94US-00192861. 98US-00133119 04-FEB-1994; 04-FEB-1994; 04-FEB-1994; 12-AUG-1998; 02-FEB-1993 18-OCT-1994 11-DEC-1995 29-JAN-1993

(CENZ ) CENTOCOR INC.

ŝ Siegel 'n Knight Ghrayeb J, Vilcek J, Daddona P,

WPI; 2002-706216/76. N-PSDB; ABS54257 Treating a neurodegenerative disease, especially multiple sclerosis, comprises administering an anti-tumor necrosis factor monoclonal antibody or its fragment

Disclosure, Fig 16B; 95pp; English.

The present invention relates to anti-tumour necrosis factor (TNF) antibodies, and anti-TNF peptides, which are specific for human tumour necrosis factor-alpha (TNFalpha). Methods of producing and uning the anti-TNF antibodies and anti-TNF peptides are also disclosed. The anti-TNF antibodies and anti-TNF peptides are also disclosed. The anti-TNF antibodies and methods of the invention are useful for treating human neurodegenerative diseases (e.g. multipple sclerosis, captified immunodeficiency syndrome (AIDS) demential complex, a demyelinating disease, acute transverse myelitis, an extrapyramidal disorder of the basal ganglia, a hyperkinetic movement disorder, a lession of the corticospinal system, a disorder of the basal ganglia, a hyperkinetic movement disorder, Parkinson's disease, progressive supranuclear palsy, a structural lesion of the crebellum, a spinocerebellar degeneration, spinal ataxia, Friedreich's ataxia, a cerbellar cortical degeneration, a multiple system degeneration, a mitochondrial multi-system disorder, demyelinating core disorder, acute transverse myelities, a disorder of the motor unit, a certebellar atrophy, anterior horn cell degeneration, amyerrophic lateral sclerosis, infantile spinal muscular atrophy, juvenile spinal muscular atrophy, Alzheimer's disease, bown's Syndrome, a diffuse Lewy muscular atrophy, alzheimer's disease, bown's Syndrome, a diffuse Lewy

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body disease, senile dementia of Lewy body type, Wernicke-Korsakoff syndrome, chronic alcoholism, Creutzfeldt-Jakob disease, subacute sclerosing panencephalitis, Hallervorden-Spatz disease, or dementia pugliistica). The present sequence represents human-murine chimeric antihuman TNPalpha (hTNPalpha) chimeric A2 (CA2) heavy chain variable region. The cA2 monoclonal anti-TNP antibody consists of mouse (from female BALB/C mice) antihuman TNP IGI antibody (designated A2), and the constant regions of human IGG1 kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour necrosis factor; monoclonal antibody; chimeric antibody; antibody;
myelodysplastic syndrome; cytostatic; vaccine.
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                                                                                                                                                                                                                                                                                                       61 HYAESVKGRFTISRDDSKSAVYLQMTDLRTEDTGVYYCSRNYYGSTYDYWGQGTTLTVS 119
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                                                                                                                                                                                                                                                                              HYAESVKGRFTISRDDSKSAVYLOMTDLRTEDTGVYYCSRNYYGSTYDYWGQGTTLTVS 119
                                                                                                                                                                                                                     1 EVKLEESGGGLVQPGGSMKLSCVASGFIFSNHWMNWVRQSPEKGLEWVAEIRSKSINSAT
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                                                                                                                                                           Length 119;
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                                                                                                                                                            100.0%; Score 636; DB 5;
100.0%; Pred. No. 1.3e-49;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                  ABP54871 standard; protein; 119
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92US-00853606.
92US-00853606.
93US-0010406.
93US-001192102.
94US-00192102.
94US-00192102.
94US-00192102.
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2001US-00927703.
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                                                                                                                                                                                         Conservative
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                                                                                                                                                                            Similarity
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                                                                                                                                  Sequence 119 AA;
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10-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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18-MAR-1992;
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Matches 119;
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16B; 97pp; English.

Fig

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region (VH) of an anti-human tumour necrosis factor (TNF) monoclonal antibody (MAb) produced by murine hybridoma line A2. A claimed method of treating a myelodysplastic syndrome in a human comprises administering an anti-TNF chimeric antibody comprising the murine A2 VH and VL (see ABP54870) regions and an IgG1 human constant region. The anti-TNF opptides and antibodies of the invention can be used in the treatment of TNF-related pathologies of the invention can be used in the treatment of pathologies, infeatmentory diseases, neurodegenerative diseases, malignant pathologies, and alcohol-induced hepatitis
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                                                                                                                                                                    100.0%; Score 636; DB 5; 100.0%; Pred. No. 1.3e-49;
                                                                                                                                                                                               Mismatches
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930S-00013413
940S-00192102
940S-00192861
950S-00324799
950S-00533119
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92US-00853606.
92US-00943852.
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(first entry)
                                                                                                                                                                                                Conservative
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N-PSDB; AAI72610.
                                                                                                                                                             Query Match
Best Local Similarity
Marches 119; Conserv
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                                                                                                                                          Sequence 119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus.
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10-JUN-2002
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11-SEP-1992
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AAB47942
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The sequences given in AAB47941-42 show the light and heavy chain variable regions of the chimeric antibody, CA2. CA2 is an anti-tumour necrosis factor (TMF) antibody. Anti-tuman TNF chimeric antibodies, may be used for treating psoriasis in humans. Psoriasis may be treated by administering: (a) anti-TNF chimeric antibody (Ab) which competitively inhibite binding of TNF to monoclonal chimeric Ab CA2; or (b) anti-TNF chimeric antibody (Ab) which competitively chimeric Ab comprising a human immunoglobulin (1g) Gl constant region and a non-human variable region, which binds to an epitope included in amino a citibody has potent TNP-inhibiting and/or neutralizing activity. Levels of CA2 as low as 125 ng/ml completely abolished the toxic activity of represented on 29-AUG-2003 to standardise OS field).
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100.0%; Pred. No. 1.3e-49;
ive 0; Mismatches 0;
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92US-00853606.
92US-000104065.
93US-00013413.
94US-00192102.
94US-00192861.
94US-00192861.
95US-00570674.
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Matches 119; Conservative
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                                                                                                                                                                                                                                                      Sequence 119 AA;
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Best Local 8
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(UYNY-) UNIV NEW YORK MEDICAL CENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour necrosis factor, TNF, antibacterial; immunosuppressive, tumour necrosis factor inhibitor; bacterial infection; cA2; sepsis; endcthelial damage; vascular damage; severe hypotension; disseminated intravascular coaqulation; shock; inflammation; bacteraemia; chimeric A2 antibody; cA2 heavy chain variable region.
                                                                                               The invention relates to an isolated nucleic acid molecule that encodes a tumour necrosis factor-alpha (TNF-alpha) specific antibody. The nucleic acid molecule is useful in diagnosing and/or treating TNF-alpha-mediated pathologies and conditions, such as bacterial, viral or parasitic lifections, chronic inflammatory diseases (e.g. Theumatoriod arthritis, Crohn's disease or ulcerative colitis), autoimmune diseases (e.g. systemic lupus erythematosus, diabetes mellitus or Grave's disease), andignancies, vascular diseases and/or neurodegenrative diseases (e.g. Alzheimer's disease) and in research purposes. The present sequence represents the amino acid sequence of the mouse TNF-alpha antibody CA2
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                                                                                                                                                                                                                                                                                                                         1 BVKLEESGGGLVQPGGSMKLSCVASGFIFSNHWRNWVRQSPEKGLEWVAEIRSKSINSAT
                               New nucleic acid molecule for diagnosing or treating tumor necrosis factor alpha-mediated diseases, e.g. infections, chronic inflammatory diseases, autoimmune diseases, cancer or neurodegenerative diseases.
                                                                                                                                                                                                                                                                                   Gaps
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                                                                            Claim 4; Fig 16B; 100pp; English.
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92US-00853606.
92US-00010406.
93US-00010406.
93US-0010203.
94US-00192093.
94US-00192093.
94US-00192097.
94US-001324799.
95US-00133119.
95US-00133119.
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2003-401678/38.
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         N-PSDB; ACA61153
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02-FEB-1993;
04-FEB-1994;
04-FEB-1994;
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18-OCT-1994;
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Mouse; TNFalpha; humanised antibody; tumour necrosis factor-alpha;
antigen; constant region; heavy chain, light chain;
antigen inding region; complementarity determining region; CDR; A2; CA2;
W framework region; complementarity determining region; CDR; A2; CA2;
W framework region; complementarity determining the activating state and the state of the stat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes a method of treating bacterial infection in a human comprising administering to the human a tumour necrosis factor (TNR)-inhibiting amount of an anti-TNF chimeric antibody, which competitively inhibites binding of TNF to monoclonal antibody cA2. The methods are useful for treating bacterial infections, a pathology associated with a sepsils (e.g. endothalial damage, vascular damage, disseminated intravascular infection, or inflammatory reaction resulting from bacterial infection, or inflammatory reaction resulting from bacteraemia. The anti-TNF antibodies and peptides in the form of pharmacceutical and/or diagnostic compounds are useful for diagnosing and treating TNF-related pathologies. This is the amino acid sequence of the chimeric A2 (CA2) antibody heavy chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                              Treating bacterial infection in a human comprises administering to the human a tumor necrosis factor (TNF)-inhibiting amount of an anti-TNF chimeric antibody, which competitively inhibits binding of TNF to
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                                                                                                                        Siegel
                                                                                                           Knight D,
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                                                                                                                 Ghrayeb
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                                                                                                                 Daddona P,
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Best Local Similarity 100.
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      monoclonal antibody cA2
                                                                                                                                                                                                                                   WPI; 2003-174129/17.
N-PSDB; ABX14787.
CENTOCOR
                                                                                                                        Vilcek J,
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The invention discloses a new humanised antibody, or its antigen-binding fragment, that selectively binds human tumour necrosis factor-alpha (Treagment, that selectively binds human tumour necrosis factor-alpha (Treagment, comprising an antigen binding region. The antibody consists of a constant region heavy or light chain of human origin and an antigen binding regions (Corss) and a framework region derived from a heavy or light chain of human origin. Also disclosed is an expression vector comprising complementarity determining regions (Corss) (fused gené encoding the humanised antibody, or its antigen-binding fragment, and the mumanised antibody, or its antigen-binding fragment, and the method for preparing it. The cytokine TWF causes proprocoagulant activity on vascular endothelial cells, increasing the adherence of neutrophils and lymphocytes and stimulating the release of platelet activaty on vascular endothelial cells, increasing the adherence of neutrophils and lymphocytes and stimulating the release of platelet activating factor from macrophages, neutrophils and vascular endothelial cells, increasing the endothelial cells. The methods and compositions are useful for the diagnosis and antibody, and antigen-binding fragment, and manufacturing a polypeptide. The methods and compositions are also useful for the diagnosis and treatment of TWF-related pathologies, such as cute and chronic inflammatory bowel disease such adverse (arbunding fragment, or disease), bacterial and viral infections including AlDS, inflammatory diseases (arboidosis, part verus host disease, scleroderma, diabetes and Grave's disease), chemical and Alzheimer's disease), conduct neovascularisation, psordissis, demonstic and antherosclerosis), neurodegenerative diseases (arboidosis, perpented is partitis, ocular neovascularisation, psordissis, decented is the murine cA2 variable heavy chain of the Fulbel method antibody
                                                                                                                                                                                                                                                                                                                                       New humanized anti-TNF antibody with an antigen binding region, useful for diagnosing and treating TNF-related pathologies, such as autoimmune disorders, bacterial and viral infections, inflammatory diseases, AIDS
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                                                                                                                                                                                                                      Le J, Vilcek J, Daddona P,
                                                                      08-JAN-2001; 2001US-00756161.
                                                                                                                   98US-00133119
                                                                                                                                                                    (UYNY ) UNIV NEW YORK STATE.
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Best Local Similarity 100.
Matches 119; Conservative
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                                                                                                                     12-AUG-1998;
                       19-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                        and cancer.
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The invention discloses a method for treating ankylosis, by administering a tumour necrosis factor (TNF)-inhibiting anti-TNF chimeric antibody competitively inhibits blinding of TNF to the murine monoclonal antibody cA2, where the antibody comprises an immunoglobulin (Ig) G1 consists of a constant region heavy or light chain of human origin and an antigen binding region, comprising complementarity determining regions corps derived from an antibody of murine origin that binds to human origin and an antigen binding region, comprising complementarity determining regions (CDRS) derived from an antibody of murine origin that binds to human origin. The creases pro-inflammatory actions which result in tissue injury, such as inducing procoagulant activity on vascular endothelial cells, increasing the adherence of activity on vascular endothelial cells, increasing the adherence of activity on vascular endothelial cells, increasing the adherence of cells. The methods and compositions are also useful for the diagnosis and the mathods including ALDS. Inflammatory chronic immune and autoimmune disorders (rheumatoid arthritis, chronic immune and autoimmune disorders (chronic disease), bacterial and viral infections including ALDS. inflammatory diseases) bacterial and viral infections including ALDS. inflammatory colliseases (sarcoidosis, chronic inflammatory bowel disease, ulcerative collitis, Crobn's disease and atherosclerosis, neurodegenerative diseases (multiple sclerosis, Parkinson's disease, dementia and Alzheimer's
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(first entry)

29-APR-2003

ABG75774;

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RESULT 13 ABG75774

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Treating ankylosis in a human, comprises administering a tumor necrosis factor (TNF)-inhibiting amount of anti-TNF chimeric antibody.

Claim 7; Fig 16B; 97pp; English.

ŝ Siegel

Daddona P, Ghrayeb J, Knight D,

WPI; 2003-255124/25. Le J, Vilcek J,

N-PSDB; ABX11366.

UYNY-) UNIV NEW YORK MEDICAL CENT.

2001US-00927703

10-AUG-2001;

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TWE inhibitor; ankylosis; anti-TWF antibody; 62; immunoglobulin Gl; IG Gl; TWF; heavy chain; light chain; antigen binding; CDR; complementarity determining region; framework region; CYCokine; pro-inflammatory; tissue injury; procoagulant; vascular endothelial cell; pro-inflammatory; tissue injury; procoagulant; vascular endothelial cell; neutrophil; lymphocyte; platelet activating factor; macrophage; immune disorder; rheumatord arthritis; thyroidosis; graft versues host disease; scleroderma; diabetes; Grave's disease; chronic inflammatory bowel disease; sarcoidosis; chronic inflammatory bowel disease; ulcerative colitis; Crohn's disease; barkinson's disease; dementia Alzheimer's disease; cancer; hepatitis; coular neovascularisation; psoriasis; duodenal ulcer; angiogenesis; female reproductive tract; haemodynamic; febrile; allergic episode.
                      Mouse; tumour necrosis factor alpha; TNFalpha; rheumatoid arthritis;
cA2 variable heavy chain of the TNFalpha antibody
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920S-00853606.
930S-00010406.
930S-00013413.
940S-00132093.
940S-00192861.
940S-00192861.
940S-00192861.
950S-00570674.
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08-JAN-2001;
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disease), cancer, hepatitis, ocular neovascularisation, psoriasis, ducdenal ulcers and angiogenesis of the female reproductive tract. The chimeric anti-TNF MAb was well-tolerated and involved no haemodynamic, febrile or allergic episodes. The sequence presented is the murine cA2 variable heavy chain of the TNFalpha antibody
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                                                                                                         Length 119;
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100.0%; Pred. No. 1.3e-49;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                           standard; protein; 119 AA.
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920S-00853606
930S-00010406
930S-00013413
940S-00192093
940S-00192861
940S-00192861
940S-00193819
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10-AUG-2001; 2001US-00927703
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                                                                                                    Query Match
Best Local Similarity 100.
Matches 119; Conservative
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N-PSDB; ACD28372.
                                                                              Seguence 119 AA;
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02-FEB-1993;
04-FEB-1994;
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04-FEB-1994;
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11-DEC-1995
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binding of TNF to monoclonal antibody (mAb) cA2; (b) chimeric anti-TNF antibody cA2; (c) at least one mAb cA2. or its TNR-binding fragment; or (d) an anti-TNF chimeric antibody with epitopic specificity identical to mAb cA2. Administering a TNF-inhibiting amount of an anti-TNF chimeric antibody which has epitopic specificity identical to mAb cA2 is useful for treating cahexia in humans, particularly a cachexia associated with cancer, HIV or AIDS. This is the maino acid sequence of mouse cA2 heavy chain variable region used in the creation of TNF alpha-antibody fusion
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100.0%; Pred. No. 1.3e-49;
ive 0; Mismatches 0;
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920S-0085366.
920S-0010406.
930S-00110408.
940S-00192102.
940S-00192102.
940S-00192861.
940S-00192861.
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2001US-00756398
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                                                                                                                                         Sequence 119 AA;
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11-SEP-1992;
11-SEP-1993;
02-FBB-1993;
04-FEB-1994;
04-FEB-1994;
18-OCT-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-DEC-1995
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                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                              ADC46572;
                                                                                                                                                                    Query Match
                                                                                                                proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                       RESULT 15
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binding fragment that competitively inhibits binding of A2 or cA2 to human TNF-alpha, useful for diagnosing and treating TNF-alpha-mediated diseases, e.g. infection.
                                                                                                                                                                                               Disclosure; SEQ ID NO 5; 97pp; English.
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The intrody or its antigen binding fragment that competitively inhibits binding of antibodies A2 or cA2 to human TNF-alpha. The invention also relates to a composition comprising the antibody or its antigen binding fragment that competitively inhibits binding of arriver, a human light or heavy chain that specifically binds human TNF-alpha, the human light or heavy chain consisting of the complementarity determining regions of the light or heavy chain of A2 or cA2, and a human light or heavy chain consisting of the complementarity determining regions of the light or heavy chain. The antibody is useful in in vivo diagnosis and therapy of TNF-alpha -mediated pathologies and conditions, such as infections (e.g. bacterial, viral, anterosclerosis), autoimmune diseases (e.g. rheumatoid arthritis, atherosclerosis), autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus erythematosus), neurodegenerative diseases (e.g. lymphomas, carcinomas) and alcohol-induced hepatitis. This sequence represents the mouse cA2 antibody heavy chain variable region polypeptide. invention relates to a human anti-tumour necrosis factor 

Sequence 119 AA;

1 EVKLEESGGGLVQPGGSMKLSCVASGFIFSNHWMWWRQSPEKGLEWVAEIRSKSINSAŢ 60 0; Gaps Query Match
100.0%; Score 636; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.3e-49;
Matches 119; Conservative 0; Mismatches 0; Indels

61 HYAESVKGRFTISRDDSKSAVYLQMTDLRIEDTGVYYCSRNYYGSTYDYWGQGTTLTVS 119  $\delta$ 

1 EVKLEESGGGLVQPGGSMKLSCVASGFIFSNHWMWWWVRQSPEKGLEWVAEIRSKSINSAT 60

В

Search completed: December 15, 2004, 17:16:39 Job time : 119.947 secs

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APPLICANT: Le, Junming
APPLICANT: Vilcek, Jan
APPLICANT: Vilcek, Jan
APPLICANT: Daddona, Peter E.
APPLICANT: Ghrayeb, John
APPLICANT: Knight, David M.
APPLICANT: Siegel, Scott A.
TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND ASSAYS EMPLOYING
TITLE OF INVENTION: ANTI-TNF ANTIBODIES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Flopped disk
MEDIUM TYPE: Flopped disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
SOUTHARE: Batentin Release #1.0, Version #1.25
SUBJECTION NUMBER: US/08/192,102
FILING DATE: 04-FEB-1994
APPLICATION NUMBER: US/08/192,093
FILING DATE: 04-FEB-1994
APPLICATION NUMBER: US 08/010,406
FILING DATE: 04-FEB-1993
APPLICATION NUMBER: US 08/010,406
FILING DATE: 12-AN11993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,852
FILING DATE: 11-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/943,852
FILING DATE: 11-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/670,827
FILING DATE: 18-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: BROOK, DAVIGE:
REGISTRATION NUMBER: 22,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08192102
Patent No. 5656272
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Lexington
STATE: Massachusetts
RESULT 1
US-08-192-102-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
  APPLII
AAPPLII
                                                                                                                                                                            December 15, 2004, 17:10:19 ; Search time 30.5398 Seconds (without alignments) 258.412 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                             636
1 EVKLEESGGGLVQPGGSMKL.....RNYYGSTYDYWGQGTTLTVS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5,
Sequence 5,
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Sequence
Sequence
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Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued_Patents_AA:*
1: /cgn2 &/ptodata1/iaa/5A_COMB.pep:*
    /cgn2 &/ptodata1/liaa/5B_COMB.pep:*
3: /cgn2 &/ptodata1/liaa/6A_COMB.pep:*
4: /cgn2 &/ptodata1/liaa/6B_COMB.pep:*
5: /cgn2 &/ptodata1/liaa/B_COMB.pep:*
6: /cgn2 &/ptodata1/liaa/PCTUS_COMB.pep:*
                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-192-102-5
US-08-192-102-5
US-08-192-81A-5
US-08-192-03A-5
US-08-192-03A-5
US-08-192-03A-5
US-08-48-340B-5
US-08-48-340B-5
US-08-767-128-28
US-08-8-224-591-14
US-08-8-224-591-14
US-08-166-093-23
US-09-166-093-23
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US-09-166-093-13
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US-09-166-094-13
US-09-166-094-13
US-09-146-094-13
US-09-443-213-13
US-09-443-213-13
US-09-443-213-13
US-09-443-213-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                    US-09-897-724-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database
                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
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Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 17, Appl Sequence 1, Appli US-09-166-093-15 US-09-16-093-15 US-09-16-015-15 US-09-16-03-13-15 US-08-392-33BA-17 US-09-166-750-17 US-09-172-019-17 US-09-172-019-17 US-09-172-019-17 US-09-172-019-17 US-09-172-019-17 US-09-172-019-17 US-09-173-17-11 US-08-448-661-1 US-08-468-661-1 US-08-468-661-1 US-08-468-661-1 US-08-468-661-1 US-08-468-661-1 US-08-468-661-1 US-08-468-671-1 US-08-468-671-1

ALIGNMENTS

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-324-799-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVKLEESGGGLVQPGGSMKLSCVASGFIFSNHWMNWVRQSPEKGLEWVAEIRSKSINSAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVKLEESGGGLVQPGGSMKLSCVASGFIFSNHWWWWVRQSPEKGLEWVAEIRSKSINSAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WESULT 2
US-06-344-799-5
US-06-344-799-5
IS Sequence 5, Application US/08324799
PRECENT No. 569312
PRECENT No. 569312
PRECENT VILORAMYION:
APPLICANT: VALORAMYION:
APPLICANT: Wilcek, Jan
APPLICANT: Wilcek, Jan
APPLICANT: Knight, David M.
APPLICANT: Massell David M.
STREET: TWO MILITA DIVE
CITY: Lexington
STREET: TWO MILITA DIVE
CITY: Lexington
STREET: TWO MILITA DIVE
CITY: Lexington
STREET: Wassachusetts
COMUTER: Ranamannetts
COMUTER: Ranamannetts
COMUTER: Ranamannetts
COMUTER: Ranamannetts
COMUTER: PROPHY disk
COMUTER: PROPHY MISSER: MASSACHUSEN
SOFTWARE: PRECENT Release #1.0, Version #1.25
SOFTWARE: PRECENT Release #1.0, Version #1.25
SOFTWARE: PRECENT NO BATA:
APPLICATION NUMBER: 04-FEB-1994
PRICH APPLICATION DATA:
APPLICATION NUMBER: 03-FEB-1994
PRICH APPLICATION DATA: 03-93
PRICH APPLICATI
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 636; DB 1; Length 119; Best Local Similarity 100.0%; Pred. No. 2.4e-55; Matches 119; Conservative 0; Mismatches 0; Indels
REFERENCE/DOCKET NUMBER: NYUS;
TELECHONINICATION INFORMATION:
TELEFAX: (617) 861-6240
TELEFAX: (617) 861-6240
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
NOLECULE TYPE: protein
US-08-192-102-5
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PRICATION DATE: 11 = MAR-1932 (1970, 437)

PRICATION DATE: 12 = MAR-1932 (1970, 437)

PRICATION DATE: 13 = MAR-1932 (1970, 437)

PRICATION: 13 = MAR-1932 (1970, 437)

PRICATION: 13 = MAR-1932 (1970, 437)

PRICATION: 140 = MAR-1932 (1970, 437)
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TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-133-119-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 HYAESVKGRFTISRDDSKSAVYLQMIDLRTEDTGVYYCSRNYYGSTYDYWGQGTTLTVS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 HYAESVKGRFIISRDDSKSAVYLQMTDLRTEDTGVYYCSRNYYGSTYDYWGQGTTLTVS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVKLEESGGGLVQPGGSMKLSCVASGFIFSNHWMNWVRQSPEKGLEWVAEIRSKSINSAT
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100.0%; Score 636; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 119; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09133119
| Patent No. 6277969
| GENERAL INFORMATION |
| APPLICANT: Us. Junming |
| APPLICANT: Vilcek, Jan |
| APPLICANT: Wilcek, Jan |
| APPLICANT: Might, David |
| APPLICANT: Knight, David |
| APPLICANT: Knight, David |
| APPLICANT: Siegel, Scott A. TITLE OF INVENTION: ANTI-THY ANTIBODIES AND PEPTIDES |
| TITLE OF INVENTION: OF HUMAN TUMOR NECROSIS. FACTOR |
| NUMBER OF SEQUENCES: 19 |
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive STREET: Two Militia Drive STREET: Two Militia Drive STATE: Assachusetts COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DAYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/133,119
FILING DATE:
                                                                                                                          NAME: Brock, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: NYU93-01M2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR AND DATA:
PRIOR THAN DATA:
APPLICATION NUMBER: 08/570,674
FILING DATE: 11-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/324,799
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,093
FILING DATE: 04-FEB-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/192,102
FILING DATE: 04-FEB-1994
FILING DATE: 04-FEB-1994
                                                      US 07/670,827
                                                                                                                                                                                                                                                                                      TYPE: amino acide TOPOLOGY: little
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 18-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-192-861A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-09-133-119-5
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FRIOR APPLICATION DATA:

PILING DATE: 302-889-1941

PRING APPLICATION NAMES: 10. 80 6/13.413

PRING APPLICATION NAMES: 10. 80 6/13.413

PRING PATE: 102-889-1932

PRING DATE: 102-889-1932

PRING DATE: 102-889-1932

PRING DATE: 102-889-1932

PRING DATE: 102-889-1932

APPLICATION NAMES: 10. 50/543,652

PRING APPLICATION NAMES: 10. 50/543,653

PRING APPLICATION NAMES: 10. 50/543,643

PRING APPLICATION NAMES
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5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVKLEESGGGLVQPGGSMKLSCVASGFIFSNHWNNWVRQSPEKGLEWVAEIRSKSINSAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 HYAESVKGRFTISRDDSKSAVYLQMTDLRTEDTGVYYCSRNYYGSTYDYWGQGTTLTVS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYAESVKGRFTISRDDSKSAVYLQMTDLRTEDTGVYYCSRNYYGSTYDYWGQGTTLTVS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                       PRIOR PILING DATE: 1993-01-29
PRIOR APPLICATION NUMBER: U.S. 08/013,413
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1992-09-11
PRIOR FILING DATE: 1992-09-11
PRIOR PILING DATE: 1992-09-11
PRIOR PILING DATE: 1992-03-18
Remaining Prior Application data removed - See File Wrapper or PALM.
SOFTWARE: PastSEQ for Windows Version 4.0
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 616; DB 4; Length 119; Best Local Similarity 100.0%; Pred. No. 2.4e-55; Matches 119; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALROW CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
CITY: BERRYVILLE
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.6%; Score 519; DB 3; Length 122;
81.3%; Pred. No. 8e-44;
Live 8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCUNTRY: USA
ZIP: 94662-8097
ZIP: 94662-8097
CCMPUTER READABLE, FORM:
MEDIUM TYPE: Floppy disk
CCMPUTER: BIM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,749A
FILING DATE: 07-UM-1995
ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL B.
REGISTRATION NUMBER: 0508.008
TELERAL (510) 601-2885
TELEPHONE: (110) 601-2885
TELEPAR: (510) 655-3542
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TELEPAR: 122 amino acids
                                          APPLICATION NUMBER: U.S. 08/010,406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08483749A Patent No. 6054561
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amino acid
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Best Local Similarity 81.3
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-483-749A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-756-301B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 HYAESVKGRFTISRDDSKSAVYLQMTDLRTEDTGVYYCSRNYYGSTYDYWGQGTTLTVS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 HYAESVKGRFTISRDDSKSAVYLQMTDLRTEDTGVYYCSRNYYGSTYDYWGQGTTLTVS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVKLEESGGGLVQPGGSMKLSCVASGFIFSNHWNWVRQSPEKGLEWVAEIRSKSINSAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 636; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 119; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Le, Junming
APPLICANT: Le, Junming
APPLICANT: Le, Junming
APPLICANT: Daddona, Peter
APPLICANT: Ghrayb, John
APPLICANT: Ghrayb, John
APPLICANT: Siegel, Scott
APPLICANT: Siegel, Scott
TITLE OF INVENTION: Human Tumor Necrosis Factor
FILE REFERENCE: 0975-1005-008
FILE REFERENCE: 0975-1005-008
CURRENT APPLICATION NUMBER: U.S. 09/133,119
PRIOR PILIONG DATE: 1998-08-12
PRIOR PLING DATE: 1998-08-12
PRIOR FILING DATE: 1998-10-18
PRIOR FILING DATE: 1998-10-18
PRIOR FILING DATE: 1998-10-18
PRIOR FILING DATE: 1998-10-18
PRIOR FILING DATE: 1994-10-18
PRIOR FILING DATE: 1994-02-04
PRIOR PLING DATE: 1994-02-04
PRIOR FILING DATE: 1994-02-04
PRIOR PLING DATE: 1994-02-04
PRIOR FILING DATE: 1994-02-04
APPLICATION NUMBER: US/08/192,093A
FILING DATE: 04-FEB-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/013,413
FILING DATE: 02-FEB-1993
PRICR APPLICATION NUMBER: US 08/010,406
FILING DATE: 29-JAN-1993
APPLICATION NUMBER: US 07/943,852
FILING DATE: 18-FE-1992
PRICR APPLICATION NUMBER: US 07/943,852
FILING DATE: 18-FE-1992
PRICR APPLICATION NUMBER: US 07/853,606
FILING DATE: 18-FE-1992
PRICR APPLICATION NUMBER: US 07/670,827
FILING DATE: 18-FE-1992
PRICR APPLICATION NUMBER: US 07/670,827
FILING DATE: 18-FE-1992
ATTORNEY AGENT INFORMATION:
NAME: BROOK, DAVIG E.
REGISTRATION NUMBER: US 07/670,827
FILING DATE: 18-FE-1992
ATTORNEY SECTION NUMBER: US 07/670,827
FILING DATE: 18-FE-1993
ATTORNEY SECTION NUMBER: US 07/670,827
FILING DATE: 18-FE-1993
ATTORNEY SECTION NUMBER: US 07/670,827
FILING DATE: 18-FE-1993
ATTORNEY SECTION NUMBER: US 07/670,827
FILING DATE: 19-940
INFORMATION FOR SECTION: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 119 anh.no acids
TYPE: amino acids
TYPE: amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09756301B Patent No. 6790444 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein US-08-192-093A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-756-301B-5
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61 HYAESVKGRFTISRDDSKSAVYLQMTDLRTEDTGVYYCSRNYYGSTYDYWGQGTTLTVS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVKLEBSGGGLVQPGGSMKLSCVASGFTFSNYMMWWVRQSPEKGLEWVAEIKLKSNNYPT
                                                                                                                                                        1 BVKLEESGGGLVQPGGSMKLSCVASGFIFSNHWMNWVRQSPEKGLEWVAEIRSKSINSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVKLEESGGGLVQPGGSMKLSCVASGFIFSNHWMWWVRQSPEKGLEWVAEIRSKSINSAT
                                                                                                            Gaps
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Patent No. 6054561
APPLICANT: NING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CENERALION
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
                                                            Score 509; DB 3; Length 120;
Pred. No. 7.5e-43;
8; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENTING SYSTEM: TC-LOUS/MS-LOUS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,749A
FILING DATE: O'-UN-1995
CLASSIFICATION: 536
ATTONERY/AGENT IRFORMATION:
NAME: SAVEREIDE, PAUL B.
REGISTRATION NUMBER: 36,914
REFRENCE/DOCKET NUMBER: 36,914
REFRENCE/DOCKET NUMBER: 36,914
TELEPRAK: (510) 601-2585
TELEPRAK: (510) 601-2585
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE (ARRACTERISTICS:
LENGTH: 114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.7%; Score 507; DB 3; 79.8%; Pred. No. 1.1e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM:PC compatible
OPERATING SYSTEM: PC_DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-08-767-128-26
'Sequence 26, Application US/08767128
'Patent No. 6111079
                                                              Query Match
Best Local Similarity 80.7%;
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 79.89
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-749A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: EMERYVILLE STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
; ORIGINAL SOURCE:
US-08-767-128-28
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                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-08-483-749A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
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                                                                                                               61 HYAESVKGRFTISRDDSKSAVYLQMTDLRTEDTGVYYCSRN----YYGSTYDYWGQGTTL 116
                                                                                                                                         61 HYAESVKGRFTISRDDSKSSVYLQLNNLRAEDTGIYYCARERYLYY--TMDYWGQGTSV 118
                                                1 EVKLEESGGGLVQPGRSWKLSCVASGFTFSNYWMWWWQSPEKGLEWVAEIRLKSNNYAT 60
                        EVKLEESGGGLVQPGGSMKLSCVASGFIFSNHWMWWRQSPEKGLEWVAEIRSKSINSAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt STREET: 3100 No. 6111079west Center, 90 South Seventh St CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                               Sequence 28, Application US/08767128

Sequence 28, Application US/08767128

GENERAL INFORMATION:
APPLICANT: WYLIE, DANNE E.
APPLICANT: WURRAY, PETER JOSEPH
APPLICANT: GOEBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLECTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-UN-1996
PRIOR APPLICATION NAMBER: PCT/US96/09258
FILING DATE: 06-UN-1995
FILING DATE: 10-OCT-1995
PRIOR APPLICATION NUMBER: 08/461,373
PRIOR APPLICATION NUMBER: 08/462,798
FILING DATE: 05-UN-1995
ATTORNEY, AGENY INPORMATION:
NAME: GATTE: 05-UN-1995
ATTORNEY, AGENY INPORMATION:
NAME: GATTE: 05-UN-1995
ATTORNEY, CARTIES 35,093
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8448.49USF1
TELECOMMUNICATION INFORMATION:
TELEFONE: 612/311-5278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FASTEX VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 120 amino acids
amino acid
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SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acidi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
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                                                                                                                                                                                                   117 TVS 119
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                                                                                                                                                                                                                                                 119 TVS 121
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US-08-392-338A-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 HYAESVKGRFTISRDDSKSAVYLQMTDLRTEDTGVYYCSRNYYGSTYDYWGQGTTLTVS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 HYAESVKGRFTISRDDSKSSVYLQMNNLRAEDTGIYYCTRYGREGGVAYWGQGTLVTVS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 BVKLEESGGGLVQPGGSMKLSCVASGPTFSNYWMNWVRQSPEKGLEWVAEVRLKS-NYAT 59
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                                                                                                                                 DB 3; Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 504.5; DB 3; Length 1 Pred. No. 2.1e-42; 7; Mismatches 14; Indels
GENERAL INFORMATION:
APPLICANT: WYLIE, DWANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOBBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morchant, Gould, Smith, Edell, Welter & STREET: 3100 No. 6111079west Center, 90 South Sever CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: SetSEQ Version 1.5
CURSIFICATION NUMBER: US/08/767,128
FILING DATE: US/08/767,128
FILING DATE: US/08/767,128
FILING DATE: US/08/767,128
FILING DATE: US/08/0956
CLASSIFICATION: 424
PRIOR APPLICATION HARS: PCT/US96
CLASSIFICATION: 424
PRIOR APPLICATION HAS:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: US-UN-1996
PRIOR APPLICATION NUMBER: US/51,373
FILING DATE: US-CT-1995
FILING DATE: US-CT-1995
FILING DATE: US-CT-1995
FILING DATE: US-CT-1995
FILING DATE: US-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: CATCET, Charles G
REGISTRATION NUMBER: 35,093
REFERRICE/DOCKET NUMBER: 35,093
REFERRICE/DOCKET NUMBER: 8648.49USF1
TELEPHONE: 612/31-578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.3%;
81.5%;
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INFORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 79.3
Best Local Similarity 81.5
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                               ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE: US-08-767-128-26
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RESULT 11 US-08-224-591-14

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APPLICANT: Whillow, Marc
APPLICANT: Wood, James F.
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
APPLICANT: Filpula, David
APPLICANT: Filpula, David
APPLICANT: Follence, Michelle
APPLICANT: Follence, Michelle
APPLICANT: Follence, Michelle
APPLICANT: Proteins
NUMBER OF SEQUENCES: 23
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVKLEESGGGLVQPGGSMKLSCVASGFIFSNHWNWWRQSPEKGLEWVAEIRSKSINSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 HYAESVKGRFTISRDDSKSAVYLOMTDLRTEDTGVYYCSRNYYGSTYDYWGQGTTLTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.6%; Score 487; DB 2; Length 242; 74.8%; Pred. No. 2.5e-40; Live 16; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, NW CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
CITY: Washington
ZITY: Washington
ZITY: U.S.A.

CONPUTE: U.S.A.

COMPUTER EDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,750
FILING DATE: 14 Erewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
RICK APPLICATION NUMBER: US 07/989,846
FILING DATE: 22-FEB-1995
RICK APPLICATION NUMBER: US 07/989,846
FILING DATE: 22-FEB-1995
RICK APPLICATION NUMBER: US 07/989,846
FILING DATE: 22-NOV-1992
RICK APPLICATION NUMBER: US 07/989,846
FILING DATE: 25-NOV-1992
RICK APPLICATION NUMBER: US 07/796,936
RILK APPLICATION NUMBER: US 07/796,936
ALELICATION NUMBER: US 08/002,845
FILING ADELE 15-0AN-1993
PRIOR APPLICATION DATE: 3-0AN-1993
APPLICATION NUMBER: US 07/980,529
FILING DATE: 20 NOV-1992
ATORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 09/7.1920002/JAG
FELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/09166750; Patent No. 6025165; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-926-789-14
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Patent No. 5990275
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Filpula, David
TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                            CZIP: 20005
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,338A
FLING DATE: 22-FEB-1995
CLASSIFICATION DATE: W 07/989,846
FLING APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FLING APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: GOLGSTEATION DATE: 29,021
REGISTRATION NUMBER: 29,021
REGISTRATION NUMBER: 29,021
REGISTRATION NUMBER: 29,021
REGISTRATION NUMBER: 29,021
RELEPAX: (202) 371-2600
TELEFAX: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
LENGTH: 24 Z MAINO acids
TYPE: AMINO acids
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CITY: Washington
STATE: 100 New York Avenue, Suite 600
STATE: 2000
STATE: 100 New York Avenue, Suite 600
STATE: 2000
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
SOFTWARE: PATENTIN NUMBER: US/08/926,789
APPLICATION NUMBER: US/08/926,789
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/224,591
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US-08-926-789-14
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Sequence 23, Application US/09166093
Sequence 23, Application US/09166093
Sequence 23, Application US/09166093
Septembarror No. 602725
APPLICANT: Whitlow, Marc APPLICANT: Hardman, Karl APPLICANT: Hilpula, David APPLICANT: Rilpula, David APPLICANT: Rollence, Michelle TITLE OF INVENTION: Multivalent Antigen-Binding Proteins NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: 23
STREET: 1100 New York Avenue, NW CITY: Washington CITY: Washington COUNTRY: D.C. CCUNTRY: D.C. CCUNTRY: D.C. CCUNTRY: D.C. CCUNTRY: D.C. CCUNTRY: D.C. CCUNTRY: CCUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.6%; Score 487; DB 3; Length 242; 74.8%; Pred. No. 2.5e-40; Live 16; Mismatches 12; Indels
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COUNTRY: U.S.A.
ZIP: 2005
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYGTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,093
PT.ING DATE: Herewith
NAME: Goldstein, Jorge A.

REFERENCE/DOCKET NUMBER: 29,021

REFERENCE/DOCKET NUMBER: 0977.003000C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEPHONE: (202) 371-2600

TELEPHONE: (202) 371-2600

REQUENCE CHARACTERRISTICS:

LENGTH: 242 amino acids

TYPE: amino acid

TYPE: amino acid

MOLBOCULE TYPE: protein

US-09-166-750-23
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REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000B
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRICE APPLICATION DATA:
APPLICATION WUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 74.8<sup>†</sup>
Matches 89; Conservative
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US-09-166-093-23
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-166-093-23
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December 15, 2004, 17:21:06 ; Search time 101.624 Seconds (without alignments) 418.250 Million cell updates/sec
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636
1 EVKLEESGGGLVQPCGSMKL.....RNYYGSTYDYWGQGTTLTVS 119
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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-10-187-121-	76-460-	-10-186-559-	-10-371-961-	.10-200-795-	-10-319-011-	-10-371-443-	-10-379-866-	-10-371-962-	0-384-060	-10-665-971-	-10-637-759-	-10-774-118-5	-10-411-037-4	-10-411-026-4	-10-410-962-4	-10-411-049-	-10-410-930-4	-10-410-997-4	-10-411-01	-10-287-994-4	-10-410-913-4	-10-384-060-2	-10-338-552-	-10-338-627-	-10-338-552-	-10-338-627-	-10-239-656-6	-10-239-656-7	-10-160-506-6	10	-10-688-015-6	
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ALIGNMENTS

JS-09-756-301A-5

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Sequence 5, Application US/09756301A
Patent No. US20010027249A1
GENERAL INPORMATION
APPLICANT: UVICeK, Jan
APPLICANT: Grayeb, John
APPLICANT: Grayeb, John
APPLICANT: Siegel, Scott
TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
TITLE OF INVENTION: Auti-TNF Antibodies and Peptides of
TITLE OF INVENTION NUMBER: U.S. 08/192,103
PRIOR FILING DATE: 1994-02-04
PRIOR PILING DATE: 1994-02-04
PRIOR FILING DATE: 1994-02-04
PRIOR PILING DATE: 1993-02-02
PRIOR APPLICATION NUMBER: U.S. 08/013,413
PRIOR PILING DATE: 1992-09-11
PRIOR PILING DATE: 1992-09-11
PRIOR PILING DATE: 1992-09-11
PRIOR PILING DATE: 1992-09-11
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Gaps

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0; Indels
        0; Mismatches
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              119; Conservative
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              Matches
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Pred. No. 2e-49;
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APPLICANT: Le, Junming
APPLICANT: Vilcek, Jan
APPLICANT: Vilcek, Jan
APPLICANT: Cardena, Peter
APPLICANT: Cardena, Peter
APPLICANT: Cardena, Peter
APPLICANT: Stegel, Coch
TILLE OF INVENTION: Human Tumor Necrosis Factor
CURRENT FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 1998-08-12
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1993-02-01
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-03-18
PRIOR FILING DATE: 1992-09-11
PRIOR APPLICATION NUMBER: U.S. 07/670,827
PRIOR FILING DATE: 1991-03-18
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                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 636; DB 9;
Best Local Similarity 100.0%; Pred. No. 2e-49;
Matches 119; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: U.S.07/670,827
PRIOR FILING DATE: 1991-03-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 119
TYPE: PRI
ORGANISM: Mus Balb/c
US-09-756-301A-5
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Sequence 5. Application US/09927703
Patent No. US2002022720A1
GENERAL INFORMATION:
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CORGANISM: Mus Balb/c
US-09-927-703-5
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                                                                                                                                                                                  61 HYAESVKGRFTISRDDSKSAVYLQMTDLRTEDTGVYYCSRNYYGSTYDYWGQGTTLTVS 119
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APPLICANT: Vilcek, Jan
APPLICANT: Vilcek, Jan
APPLICANT: Daddona, Peter
APPLICANT: Gladdona, Peter
APPLICANT: Siegel, Scott
TILE OF INVENTION 'Anti-TNF Antibodies and Peptides of
TILLE OF INVENTION 'Anti-TNF Antibodies and Peptides
CURRENT APPLICATION 'Anti-TNF Antibodies and Peptides
CURRENT FILING DATE: 1998-08-12
PRIOR FILING DATE: 1998-08-12
PRIOR FILING DATE: 1998-08-12
PRIOR FILING DATE: 1998-08-12
PRIOR FILING DATE: 1998-02-04
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-03-18
PRIOR PRIOR FILING DATE: 1993-03-18
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100.0%; Score 636; DB 9; Length 1:
Best Local Similarity 100.0%; Pred. No. 2e-49;
Matches 119; Conservative 0; Mismatches 0; Indels
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US-09-756-161A-5
; Sequence 5, Application US/09756161A
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61 HYAESVKGRFTISRDDSKSAVYLQMTDLRTEDTGVYYCSRNYYGSTYDYWGQGTTLTVS 119
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US-09 997-724
US-09 997-724
Publication No US20030175837A1
GENERAL INFORMATION:
APPLICANT: Le, Junming
APPLICANT: Le, Junming
APPLICANT: Le, Junming
APPLICANT: Vilcek, Jan
APPLICANT: Alaqeb, John
APPLICANT: Siegel, Scott
TITLE OF INVENTION: Human Tumor Necrosis Factor
CURRENT APPLICANTON NUMBER: U.S. 08/192,093
PRIOR FILING DATE: 1993-02-04
PRIOR FILING DATE: 1993-01-29
PRIOR APPLICATION NUMBER: U.S. 08/013,413
PRIOR FILING DATE: 1993-09-11
PRIOR FILING DATE: 1992-09-11
PRIOR APPLICATION NUMBER: U.S. 07/670,827
PRIOR APPLICANTON NUMBER: U.S. 07/670,827
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0; Mismatches (
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: U.S. 08/570,674
PRIOR PILING DATE: 1995-12.1
PRIOR PILING DATE: 1995-12.1
PRIOR APPLICATION NUMBER: U.S. 08/324,799
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1993-02-04
PRIOR FILING DATE: 1993-02-04
PRIOR FILING DATE: 1993-02-04
PRIOR FILING DATE: 1993-01-29
PRIOR FILING DATE: 1993-01-29
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1992-09-11
PRIOR FILING DATE: 1992-09-18
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100.0%; Pred. No. 26
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Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Mus Balb/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-756-398B-5
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                                                                                    APPLICANT: Le, Jumning
APPLICANT: Le, Jumning
APPLICANT: Vilcek, Jan
APPLICANT: Carden, Peter
APPLICANT: Grayeb, John
APPLICANT: Grayeb, John
APPLICANT: Right, David M.
APPLICANT: Siegel, Scott
TITLE OF INVENTION: Human Tumor Necrosis Factor
CURRENT APPLICATION NUMBER: US, 09/133,119
PRIOR PELING DATE: 1998-08-12
PRIOR PELING DATE: 1998-08-12
PRIOR PELICATION NUMBER: U.S. 08/192,799
PRIOR PELICATION NUMBER: U.S. 08/192,093
PRIOR PELICATION NUMBER: U.S. 08/010,406
PRIOR PELICATION NUMBER: U.S. 08/013,413
PRIOR PELICATION NUMBER: U.S. 08/013,413
PRIOR PELICATION NUMBER: U.S. 07/943,852
PRIOR PELICATION NUMBER: U.S. 07/670,827
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APPLICANT: Le, Junming
APPLICANT: Le, Junming
APPLICANT: Daddona, Peter
APPLICANT: Glass, John
APPLICANT: Knight, David M.
APPLICANT: Knight, David M.
APPLICANT: Siegel, Scott
TITLE OF INVENTION: Anti-TYP Antibodies and Peptides of
TITLE OF INVENTION: Human Tumor Necrosis Factor
FILE REFERENCE: 0975.1005-006
CURRENT FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: U.S. 09/133,119
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100.0%; Pred. No. 2e-49;
tive 0; Mismatches C
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Best Local Similarity 100.
Matches 119, Conservative
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US-09-756-161A-5
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                                                                                                                100.0%; Score 636; DB 10; Length 119; 100.0%; Pred. No. 2e-49; ive 0; Mismatches 0; Indels 0
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US-10-043-450-5

Sequence 5, Application US/10043450

Publication No. US20020141996A1

GENERAL INFORMATION:

APPLICANT: Vicek, Jan

APPLICANT: Wilcek, Jan

APPLICANT: Girayeb, John

APPLICANT: Right, David M.

APPLICANT: Right, David M.

APPLICANT: Siegel, Scott

TITLE OF INVENTION: Human Tumor Necrosis Pactor

FILE REFERENCE: 0975.1005-013

FURRENT APPLICANT: NUMBER: US/10/043,450

CURRENT FILING DATE: 2002-01-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Le, Junming
APPLICANT: Loidek, Jan
APPLICANT: Vilcek, Jan
APPLICANT: Daddona, Peter
APPLICANT: Ghrayeb, John
APPLICANT: Knight, David M.
APPLICANT: Siegel, Scott
TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
TITLE OF INVENTION: Human Tumor Necrosis Factor
FILE REPERENCE: 0975.1005-013
CURRENT APPLICATION NUMBER: US/10/010,229
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US/09/927,703
PRIOR PLING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/10010229
Publication No. US20020114805A1
GENERAL INFORMATION:
                                                                                                             Query Match
Best Local Similarity 100.0
Matches 119; Conservative
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Best Local Similarity 100.
Matches 119; Conservative
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-897-724-5
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ORGANISM: Mus Balb/c
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
US-10-010-229-5
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LENGTH: 119
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US-10-010-229-5
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61 HYAESVKGRFTISRDDSKSAVYLQMTDLRTEDTGVYYCSRNYYGSTYDYWGQGTTLTVS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Let, Junming
APPLICANT: Let, Junming
APPLICANT: Vilcek, Jan
APPLICANT: Glargeb, John
APPLICANT: Glargeb, John
APPLICANT: Siegel, Sock
TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
TITLE OF INVENTION: Anti-TNF Antibodies
FILE REPERENCE: 3002-07-29
CURRENT FILING DATE: 2001-01-08
PRIOR FILING DATE: 1996-10-12
PRIOR PELICATION NUMBER: U.S. 08/192,093
PRIOR PELICATION NUMBER: U.S. 08/013,413
PRIOR PELICATION NUMBER: U.S. 08/013,413
PRIOR PELICATION NUMBER: U.S. 08/013,413
PRIOR APPLICATION NUMBER: U.S. 08/013,413
PRIOR APPLICATION NUMBER: U.S. 08/013,413
PRIOR APPLICATION NUMBER: U.S. 08/013,413
PRIOR PELICATION NUMBER: U.S. 08/013,413
PRIOR APPLICATION NUMBER: U.S. 08/013,413
PRIOR APPLICATION NUMBER: U.S. 08/013,413
PRIOR APPLICATION NUMBER: U.S. 08/013,413
PRIOR PELICATION NUMBER: U.S. 08/013,413
PRIOR PELICATION NUMBER: U.S. 08/013,413
PRIOR APPLICATION NUMBER: U.S. 08/013,413
PRIOR PELICATION NUMBER: U.S. 08/013,413
PRIOR PELICATION NUMBER: U.S. 08/013,413
PRIOR PELICATION NUMBER: U.S. 08/013,413
PRIOR APPLICATION NUMBER: U.S. 08/013,413
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NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
EDNGTH: 119
TYPE: PRT
       PRIOR APPLICATION NUMBER: U.S. 07/943,852
PRIOR FILING DATE: 1922-09-11
PRIOR PILING DATE: 1992-03-18
PRIOR PILING DATE: 1992-03-18
PRIOR PILING DATE: 1992-03-18
PRIOR PILING DATE: 1991-03-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SCOT ID NO 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/10208145
Publication No. US20030133935A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CRGANISM: Mus Balb/C
US-10-043-432-5
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL PETER GENERAL FORCE
APPLICANT: GENERAL DAVID
APPLICANT: GENERAL DAVID
APPLICANT: Knight, David M.
APPLICANT: NOTE:
TITLE OF INVENTION: Human Tumor Necrosis Factor
FILE REFERENCE: 0975.1005.013
CURRENT APPLICATION NUMBER: US/10/43,432
CURRENT APPLICATION NUMBER: US.
PRIOR PILING DATE: 2001-01.09
PRIOR PILING DATE: 1998-08-12
PRIOR FILING DATE: 1998-10-18
PRIOR FILING DATE: 1994-10-18
PRIOR FILING DATE: 1994-10-18
PRIOR FILING DATE: 1994-02-04
PRIOR PLING DATE: 1994-02-04
PRIOR APPLICATION NUMBER: U.S. 08/192,093
PRIOR PLING DATE: 1994-02-04
PRIOR PLING DATE: 1993-02-04
PRIOR PLING DATE: 1993-02-04
PRIOR PLING DATE: 1993-02-04
PRIOR PLING DATE: 1993-02-04
PRIOR PLING DATE: 1993-02-06
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100.0%; Pred. No. 2e-49;
ative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: U.S. 08/192,102
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1994-02-04
PRIOR APPLICATION NUMBER: U.S. 08/192,093
PRIOR PILING DATE: 1994-02-04
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1993-01-29
PRIOR PRIOR PILING DATE: 1993-01-29
PRIOR PRIOR DATE: 1993-01-29
PRIOR PRIOR DATE: 1993-02-02
PRIOR PRIOR DATE: 1993-02-02
PRIOR PRIOR DATE: 1993-03-18
PRIOR FILING DATE: 1992-03-18
PRIOR FILING DATE: 1992-03-18
PRIOR FILING DATE: 1992-03-18
PRIOR FILING DATE: 1991-03-18
NUMBER OF SEQ 1D NOS: 19
SEQ 1D NO 5
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Publication No. US20030054004A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 119; Conservative
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TYPE: PRT
ORGANISM: Mus Balb/c
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No. US20030147891A1
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                                  0; Gaps
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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US-10-198-845-5
Sequence 5, Application US/10198845
Publication No. US20030144484A1
GENERAL INFORMATION:
APPLICANT: Le, Junming
APPLICANT: Genave Peter
APPLICANT: Girayeb, John
APPLICANT: Girayeb, John
APPLICANT: Siegel, Scott
TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
TITLE OF INVENTION: MUMBER: US/10/198,845
CURRENT FILING DATE: 2002-01-08
FRICK FILING DATE: 1998-08-12
FRICK PILING DATE: 1998-08-12
FRICK PILING DATE: 1998-08-12
FRICK PILING DATE: 1998-08-12
FRICK PILING DATE: 1994-02-04
FRICK PILING DATE: 1994-02-04
FRICK APPLICATION NUMBER: U.S. 08/192,093
FRICK FILING DATE: 1994-02-04
FRICK APPLICATION NUMBER: U.S. 08/192,093
FRICK FILING DATE: 1993-01-29
FRICK FILING DATE: 1992-09-11
FRICK FILING DATE: 1992-09-11
FRICK FILING DATE: 1992-09-11
   Best Local Similarity 100.0%; Pred. No. 2e-49;
Matches 119; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 119; Conservative
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; TYPE: PRT
; ORGANISM: Mus Balb/c
US-10-198-845-5
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RESULT 13 US-10-227-488-5 ; Sequence 5, Application US/10227488

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| MEDICANT | MILLS | MEDICANT | MILLS | MEDICANT | MEDICANT | MEDICANT | MEDICANT | MEDICANT | MILLS | MEDICANT | MIRBS | MEDICANT | MEDICANT | MIRBS | MEDICANT | MI
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1 EVKLEESGGGLVQPGGSMKLSCVASGFIFSNHWMWWRQSPEKGLEWVAEIRSKSINSAT 60
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100.0%; Pred. No. 2e-49;
tive 0; Mismatches 0; Indels 0
          PRIOR PILLING DATE: 1994-02-04
PRIOR APPLICATION NUMBER: U.S. 08/192,093
PRIOR PILLING DATE: 1994-02-04
PRIOR PILLING DATE: 1993-01-29
PRIOR FILLING DATE: 1993-01-29
PRIOR FILLING DATE: 1993-01-29
PRIOR PILLING DATE: 1993-02-02
PRIOR PILLING DATE: 1993-02-03
PRIOR PILLING DATE: 1992-09-11
PRIOR PILLING DATE: 1992-03-18
PRIOR PILLING DATE: 1992-03-18
PRIOR PILLING DATE: 1991-03-18
PRIOR PILLING DATE: 1991-03-18
PRIOR FILLING DATE: 1991-03-18
NUMBER OF SEQ ID NOS: 19
SOFFWARE: FASISEQ for Windows Version 4.0
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Best Local Similarity 100.0
Matches 119; Conservative
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CORGANISM: Mus Balb/c
US-10-176-460-5
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100.0%; Score 636; DB 14; Length 119;
Best Local Similarity 100.0%; Pred. No. 2e-49;
Matches 119; Conservative 0; Mismatches 0; Indels 0
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USAGuence 5, Application US/10176460

Publication No. US20030176676A1

Sequence 5, Application US/10176460

Publication No. US20030176676A1

APPLICANT: Vicek, Jan

APPLICANT: Vicek, Jan

APPLICANT: Siegel, Scott

ITLE OF INVENTION: Anti-TNF Antibodies and Peptides of

ITLE OF INVENTION: Anti-TNF Antibodies and Peptides of

ITLE OF INVENTION: Anti-TNF Antibodies and Peptides of

ITLE OF INVENTION: Auti-TNF Anti-TNF Antibodies

PRICR PELICATION NUMBER: US/10/176,460

CURRENT FILING DATE: 1998-10-10

PRIOR PILING DATE: 1998-10-11

PRIOR PILING DATE: 1998-10-18

PRIOR FILING DATE: 1994-10-18

PRIOR PILING DATE: 1994-10-18

PRIOR PILING DATE: 1994-10-04

PRIOR PILICATION NUMBER: U.S. 08/192,102

PRIOR PILING DATE: 1994-10-04

PRIOR PILING DATE: 1994-10-04

PRIOR PILING DATE: 1994-10-06
CURRENT FILING DATE: 2002-06-28

PRIOR APPLICATION NUMBER: US 09/756,398

PRIOR PILING DATE: 2001-01-08

PRIOR PLING DATE: 1980-08-12

PRIOR APPLICATION NUMBER: U.S. 08/570,674

PRIOR APPLICATION NUMBER: U.S. 08/570,674

PRIOR PILING DATE: 1998-08-12

PRIOR PILING DATE: 1998-08-12

PRIOR PLING DATE: 1994-02-04

PRIOR PLING DATE: 1994-02-04

PRIOR PLING DATE: 1994-02-04

PRIOR PLING DATE: 1994-02-04

PRIOR PRIOR DATE: 1994-02-04

PRIOR PLING DATE: 1994-02-04

PRIOR PLING DATE: 1994-02-04

PRIOR PLING DATE: 1993-01-29

PRIOR PLING DATE: 1993-01-29

PRIOR PLING DATE: 1993-02-02

PRIOR PLING DATE: 1993-02-02

PRIOR PLING DATE: 1993-02-03

PRIOR PLING DATE: 1992-03-18

PRIOR PLING DATE: 1991-03-18

NUMBER: OF SECIENT NUMBER: U.S. O7/670,827

PRIOR PLING DATE: 1991-03-18

NUMBER: OF SECIENT NUMBER: U.S. O7/670,827

PRIOR PLING DATE: 1991-03-18
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; TYPE: PRT
; ORGANISM: Mus Balb/c
US-10-187-121-5
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Appeades: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C.Accession: C92811, A02072
J. Immunol. 128, 302-307, 1982
A.Filter: The complete V domain amino acid sequences of two myeloma inulin-binding protental roomplete V domain amino acid sequences of two myeloma inulin-binding protental roomplete V domain amino acid sequences of two myeloma inulin-binding protental roomplete V domain amino acid sequences of two myeloma inulin-binding protental roomplete V domain amino acid sequences: This complete V domain amino CSS - references: UNIPROT: P01801
C.Superfamily: immunoglobulin was isolated from a myeloma protein that binds inulin.
C.Superfamily: immunoglobulin homology clambal homology checkeywords: heterotetramer; immunoglobulin homology clambal F:15-100/Domain: immunoglobulin homology clambal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
(29380
Ig heavy chain precursor V region (BC-1004) - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Accession: (329380
C.Accession: (329380
R.Accession: 222, 13579-13583, 1987
A.Title: Nucleotide and translated amino acid sequences of cDNA coding for the vAreterace number: A92612; NUID:88007582; PMID:3115981
A.Accession: (329380
A.Molecule type: mRNA
A.Reterace number: A92612; NUID:88007582; PMID:3115981
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F;34-119/Domain: immunoglobulin homology < IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 EVKLEESGGGIVQPGGSMKLSCAASGFTFSDAWYDWVRQSPEKGLEWVAELRSKAHNHAT
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    13; Indels
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Pred. No. 1.5e-38;
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; Pred. No. 2.5e-39;
11; Mismatches 13;
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                                          $31678
$31587
132513
$12953
$23624
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S78486
A41940
AVMS63
F30539
S20775
G1MS21
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79.8%;
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81.5%;
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Best Local Similarity 79.84
Matches 95; Conservative
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(c) 1993 - 2004 Compugen Ltd.
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Awnsol, Tegion (U61) - mouse C;Species: Mus musculus (house mouse)
C;Accession: B93818; A02072
R;Vrana, M.; Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. US.A. 75, 1957-1961, 1978
A;Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
A;Reference number: A93818; MUID:78158406; PMID:417344
A;Accession: B93818
A;Molecule type: protein
A;Residues: 1.113 <VRA>
A;Cross-references: UNIPPROT:P01797
C;Comment: This chain was isolated from a myeloma protein that binds inulin.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Comment: immunoglobulin homology closy clo
                                                                                                                                                                                                                                                                                                                                                                                                      inulin-binding myeloma protein.
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61 HYAESVKGRFTISRDDSKSSVYLRMNNLRPEDTGIXYCT----TGFAYWGQGTLVTVS 114
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Local Similarity 80.5%; Pred. No. 1.1e-37;
es 95; Conservative 8; Mismatches 10;
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Ig heavy chain V region (2S1.3)
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A39818; A02072
R;Vrana, M.; Rudikoff, S.; Porter, M.
Proc. Natl. Acad. Sci. US.A. 75, 1957-1961, 1978
A;Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
A;Reference number: A93818; MUID:78158406; PMID:417344
A;Accession: A93818
A;Molecule type: protein
A;Residues: 1-113 «VRA»
A;Cross-references: UNIPROT:P01796
C;Comment: This chain was isolated from a myeloma protein that binds inulin.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Gomment: This chain was isolated from a myeloma protein inmunoglobulin homology simm.
F;15-100/Domain: immunoglobulin homology simm.
F;22-98/Disulfide bonds: #status predicted
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                                                                                                                                                 1 EVKLEESGGGLVQPGGSMKLSCVASGFTFSNYWMNWVRQSPEKGLEWVAEIRLKSNNYAT 60
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                                                                                 1 EVKLBESGGGLVQPGGSMKLSCVASGFIFSNHWMWWRQSPEKGLEWVAEIRSKSINSAT
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                     9; Indels
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1 Similarity 81.4%; Pred. No. 3.2e-38;
96; Conservative 8; Mismatches 9.
                     8; Mismatches
                        97; Conservative
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Best Local S
Matches 96
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Tarleary chain V-III region (HPC76) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1980 #sequence_revision 30-Sep-1980 #text_change 09-Jul-2004
C;Accession: A02074
R;Bernard, O.; Gough, N.M.
R;Bernard, O.; Gough, N.M.
A;Title: Nucleotide sequence of immunoglobulin heavy chain joining segments between trans, A;Reference number: A02074; MUID:81013937; PMID:6251474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain precursor V region (mAb H8) - mouse (fragment)
(Species: Mus musculus (house mouse)
(Species: Nus musculus (house mouse)
(Spacession: Polls)
(Spacession: Polls)
(Shong, H.J.; Kim, A.K.; Ryu, C.J.; Park, S.S.; Chung, H.K.; Kwon, K.S.; Kim, K.L.; Kim
(Gene 121, 331-335, 1992)
(A) Title: Cloning and characterization of CDNAs coding for heavy and light chains of a mount of the chain of the ch
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A,Molecule type: mRNA
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Fesidues: 1-111 < BER>
A,Cross-references: UNIPROT:P01804
A,Note: the sequence was also determined from the differentiated gene
A,Note: the sequence of the first 197 residues of the C region was also determined and
C,Superfamily: immunoglobulin v region; immunoglobulin homology
C,Reywords: heterotetramer; immunoglobulin
F;10-94/Domain: immunoglobulin homology <IMM>
F;10-94/Domain: immunoglobulin predicted
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                                                                  binds inulin
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A; Residues: 1-139 < HON.
A; Cross-references: GB:M98041; NID:g195092; PIDN:AAA38159.1; PID:g195093
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
C; Keywords: heteroterramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-139/Product: Ig heavy chain V region #status predicted <MAT>
F;34-119/Domain: immunoglobulin homology <IMM>
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    A,Cross-references: UNIPROT:P01798
C;Comment: This chain was isolated from a myeloma protein that I
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
F;22-98/Disulfide bonds: #status predicted
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; Pred. No. 2.5e-37;
11; Mismatches 9;
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Pred. No. 4.3e-37;
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Best Local Similarity
Matches 93; Conserv
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Matches 93; Conserv
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                                                                       C; Accession: A25803
R; Herbst, H.; Grutter, T.; Aebersold, R.; Braun, D.G.
Biol. Cham. Hoppe-Seyler 367, 843-851, 1986
A; Title: The complete amino-acid sequence of the variable domain of a monoclonal anti-st A; Reference number: A25803; MUID:87076047; PMID:3539142
A; Accession: A25803
A; Accession: A25803
A; Residues: 1-115 chrex-
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterocteramer; immunoglobulin
F; 15-100/Domain: immunoglobulin homology < IMM>
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Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996
Accession: A25803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ig heavy chain V-III region (E109) - mouse Cispecies: Mus musculus (house mouse) Cispecies: Mus musculus (house mouse) Cispecies: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004 Cist Cispecies 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004 Cist Cispecies in Cispecies in Cispecies in Sequence of Cispecies in Sequence variation among heavy chains from inulin-binding myeloma payateles. Sequence variation among heavy chains from inulin-binding myeloma payacession: C9388 Aixolecule type: protein Aixolecule type: protein Aixolecule type: 1-113 <VRA>
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Pred. No. 2e-37;
7; Mismatches 11;
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Pred. No. 1.4e-37;
7; Mismatches 13
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80.5%;
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Best Local Simil
Matches 95;
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Matches
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61 YYSDSVKGRFTISRDDSKSSVYLQMNNLRVEDMGIYYCTGSYYG--MDYWGQGTSVTVS 117
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Best Local Similarity
Matches 88; Conserv
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Best Local S:
Matches 93
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The first of the first 
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[Cispeciae: Mus musculus (house mouse)
Cispeciae: Mus musculus (house mouse)
Cipate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
A;Reference number: 838713
A;Residues: 19-115 *CINA
A;Residues: 1-115 *CINA
A;Residues: 1-115 *CINA
A;Residues: 1-115 *CINA
A;Residues: 1-115 *CINA
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;14-99/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VKLVESGGGLVQPGGSMKLSCVASGFTFSSYMMSWVRQSPEKGLEWIAEIRLKSDNYATH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YAESVKGKFTISRDDSKSRLYLOMNSLRAEDTGIYYCT----ARLGDYWGQGTTLTVS 114
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                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                         VKGRFIISRDDSKSSVYLQMMNLRAEDTGIYYCTR---PGVPDYWGQGTTLTVS 110
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                                                 Score 489; DB 1; Length 111;
Pred. No. 9.3e-37;
5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.6%; Score 487; DB 2; Length 11
74.8%; Pred. No. 1.5e-36;
ive 16; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 488; DB 2; Length 11:
Pred. No. 1.2e-36;
8; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.7%; Score 488;
                                                            Query Match
Best Local Similarity 83.3%;
Matches 95; Conservative
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nes 89; Conservative
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ly heavy chain V region (AMPC1) - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus Mug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C; Accession: A02073
R; Rudikoff, S.; Potter, M.
J; Immunol. 127, 191-194, 1981
A; Tille: Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a n. A; Reference number: A92810; MUID:81216632; PMID:6787122
A; Accession: A02073
A; Molecule type: protein
A; Residues: 1-113 - RUD>
A; Residues: 1-13 - RUD>
A; Residues: UNIPROT: P01803
A; Rosserences: WIRPROT: P01803
C; Comment: This chain was isolated from a myeloma protein that binds inulin.
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology xIMM>
F; 12-100; Domain: immunoglobulin homology xIMM>
F; 22-98/Disulfide bonds: #status predicted
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R.Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
R.Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
R.Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
R.Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie A; Reference number: 809955; MUID:90269328; PMID:2347362
A; Recession: 809958
A; Residues: 1-121 «REI»
A; Residues: 1-121 «REI»
A; Residues: BMEL:X51846; NID:955246; PIDN:CAA36139.1; PID:9930214
C; Superfamily: immunoglobulin vegion; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 YAESVKGRFTISRDDSRSRVYLOMNSLRAEDTGIYYCTGNHYYGXSFAYWGQGTLVTAS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVKLEESGGGLVQPGGSMKLSCVASGFIFSNHWNNWVRQSPEKGLEWVAEIRSKSINSAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVKLEESGGGLVQPGRSMKLSCVASGFTFSNYWWNWVRQSPEKGLEWVAEIRLKSHNYAI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V-D-J region (1E10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VKLEESGGGLVQPGGSMKLSCVASGFIFSNHWNNWVRQSPEKGLEWVAEIRSKSINSATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.6%; Score 480.5; DB 1.
78.8%; Pred. No. 5.4e-36;
tive 7; Mismatches 13
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73.9%; Pred. No. 4.5e-35;
tive 12; Mismatches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93; Conservative
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STRAIN-FVBN, TISSUE-Colon,

STRAIN-FVBN, TISSUE-Colon,

MEDLINE-2388257, Pubbled=12477932,

MEDLINE-2388257, Pubbled=12477932,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Blata N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Heish F.,

B pietchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A stapleton M., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,

B brownstein M.J., Usdin T.B., Tockhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rabask S.A., McEwan P.-J., McKernan R.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

Richards S., Worley W., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan, A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Morise A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

and moning chola mad initial analysis of more than 15,000 full-length human

The strain of the stra
  Bad00406 camelus d
Bad00520 camelus d
Aal35882 lama glam
P01790 mus musculu
Bad0030 camelus d
Q9191 homo sapien
Bad00435 camelus d
Q6gm/2 homo sapien
G6gm/2 mus musculu
G6gm/2 mus musculu
                                                                                                                                                                                                                     Cag34081 mus muscu
Bad00469 camelus d
Bad00405 camelus d
                                                                                                                                                                                                                                                                                             Ofp6c4 homo sapien
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Straubberg R.;
Straubberg R.;
Straubberg R.;
Straubberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO49143; AAH49143.1; -.
RSSP; P01789; MMP.
InterPro; IPR00110; Ig-1ike.
InterPro; IPR003597; Ig cl.
InterPro; IPR003596; Ig whc.
InterPro; IPR003596; Ig whc.
InterPro; IPR0047; ig l.
SMART; SM00406; IGv; I.
PROSITE; PS00290; IG WHC; UNKNOWN_2.
PROSITE; PS00290; IG WHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 487 AA; 53019 MW; 31F2C893900A4D80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus (Mouse).
Eukarvote: Mar. Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      487 AA
                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                          AAL35882
HV21 MOUSE
BAD00530
                                                                                                         Q9UL91
BAD00435
Q99KA4
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OGKB05
CAG34081
BAD00469
BAD00405
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SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
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Q80ZI7
  AC TO THE SECOND SECOND
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Aah41037 homo sapi
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                                                                                                                                            December 15, 2004, 17:01:54 ; Search time 132.164 Seconds (without alignments) 518.066 Million cell updates/sec
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Bad00404 camelus
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                                                                                                                                                                                                                                                                                  1 EVKLEESGGGLVQPGGSMKL.....RNYYGSTYDYWGQGTTLTVS
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                           1825181 seqs, 575374646 residues
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HV30_MOUSE
TV28_MOUSE
V31_MOUSE
35_MOUSE
35_MOUSE
4_MOUSE
77_RAT
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QEGMX2
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Maximum Match 100%
Listing first 45 summaries
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HV20_MOUSE
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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636
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Match Length DB
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protein that

Query Match Best Local &

Matches

61

g 8 g 6 9 HV32 MOUSE

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1 EVKLEESGGGLVQPGGSMKLSCVASGFIFSNHWMWWVRQSPEKGLEWVAEIRSKSINSAT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Johnson N., Slankard J., Paul L., Hood L.;
Johnson N., Slankard J., Paul L., Hood L.;
Johnson N., Slankard J., Paul L., Hood L.;
"The complete V downin amino acid sequences of two myeloma inulin-
binding proteins",
J. Immunol. 128:302-307 (1982).
J. Immunol. 128:302-307 (1982).
J. SIMILANEOUS: This chain was isolated from a myeloma protein that
JINGCELLANEOUS: This chain immunoglobulin-like domain.
PIR, D92811, AWMS82.
HSSP: P01852; INFO.
InterPro; IPRO7110; Ig-like.
InterPro; IPRO7110; Ig-like.
Finent PROAM7: A., 19-V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 HYAESVKGRFTISRDDSKSSVYLQMNLRAEDTGIYYCT-----TGFAYWGQGTLVTV 113
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                           MEDLINE=78158406; PubMed=417344;
Vrana M., Rudikoff S., Potter M.;
"Sequence variation among heavy chains from inulin-binding myeloma
Ig heavy chain V-III region A4.
Mus musculus (Mouse).
Was huscalus (Mouse).
Wararyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).

1- MISCELLANEOUS: This chain was isolated from a myeloma prot binds inulin.

1- SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR, A93818; AVWSAB.

RISS, POLTAS, 11GC.

7 InterPro; IPRO01596; Ig_v.

8 Fram, PRO041; ig; 1.

8 FRART; SMO0406; IGV; 1.

8 PROSITE; PSS00835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.5%; Score 505.5; DB 1; Length 81.4%; Pred. No. 6.2e-43; ive 8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 113
113 AA; 12675 MW; 76658C121C598285 CRC64;
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SMART; SM0046; ig; 1.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
DOMAIN 1 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct protein sequencing; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig-like.
By similarity.
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MEDLINE=82099361; PubMed=6798111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 81.4 ses 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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SEQUENCE
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P01802;
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                                                                                                                                                                                                                                                                         80 HYAESSVKGRFTISRDDSKSSVYLQMNNLRAEDTGIYYCTRRGYGDFNWYFDVWGAGTTVT 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVKLEESGGGLVQPGGSMKLSCVASGFTFSNYWMNWVRQSPEKGLEWVAEIRLKSNNYAT 60
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 44, Last annotation update)
19 heavy chain v-III region J606.
Mus musculus (Mouse).
Mammalia, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnson N., Slankard J., Paul L., Hood L., "The complete V domain amino acid sequences of two myeloma inulin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ľ,
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                                                Length 487;
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115 115
115 AA; 12810 MW; B67AD6638A121ASF CRC64;
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SMART; SM00406; IGv; 1.
PROSITE; PSS0835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
DOMAIN
                                          81.1%; Score 515.5; DB 2;
79.5%; Pred. No. 3.2e-43;
iive 9; Mismatches 13;
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81.5%; Pred. No. 2.5e-43;
Live 8; Mismatches 9;
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(Rel. 01, Last sequence update)
(Rel. 44, Last annotation update)
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By similarity.
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MEDLINE=82099361; PubMed=6798111;
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97; Conservative
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Best Local Similarity
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HV27 MOUSE
ID HV27 MOUSE
AC P01796;
DT 21-UUL-1986 (
DT 05-UUL-1996
DT 05-UUL-2004 (
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P01801;
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XI TISSUE-Mammary tumor metastatized to lung. Tumor arose spontaneously;

XI STURE-22388257; PubMed=12477932;

XI STURE-22388257; PubMed=12477932;

XI Altschul S. F., Collins F.S., Wargner L., Shenmen C.M., Schuler G.D.,

Altschul S. F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsiah F.,

A platchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

A platchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

A platchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,

A platchenko L., Modin T.B., Toehiyuki S., Carninol E.,

Brownstein M.J., Uddin T.B., Toehiyuki S., Abramson R.D., Millahy S.J.,

Bosak S.A., McEwan P.J., NCKernan K.J., Malek J.A., Gunaratne P.H.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villaton D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Rhey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rheighez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

" Generation and initial analysis of more than 15,000 full-length human
                                                                         ij
                                                                                                  1 EVKLBESGGGLVQPGGSMKLSCVASGFIFSNHWWNWVRQSPEKGLEWVAEIRSKSINSAT 60
                                                                                                                   EVILEESGGGLVQPGGSMKLSCVASGFTFSNYWMNWVRQSPEKGLEWVAEIRLKSHNYAT 60
                                                                                                                                                             HYAESVKGRFTISRDDSKSAVYLQMTDLRTEDIGVYYCSRNYYGSTYDYWGQGTTLTVS 119
                                                                                                                                                                           61 HYAESSVKGRFTISRDDSKSSVYLRMNURPEDTGIYYCT----TGFAYWGQGTLVTVS 114
                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                       5;
                                          Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Straubberg R.;
Submitted (UUN-2002) to the EMBL/GenBank/DDBJ databases.
R InterPro; IPR003599; 19.
R Ffam; PP07544; C1-set; 3.
R Ffam; PP07654; C1-set; 3.
R SMART; SM00409; 1G; 2.
R SMART; SM00409; 1G; 2.
R RARRI; SM00409; 1G; 2.
R RARRI; SM00409; 1G; 2.
R RARRI; SM00409; 1G; 10.
R RARRI; SM00409; 1G; 10.
R ROSITE; PS50039; 1G ILKE; 4.
R ROSITE; PS50039; 1G ILKE; 4.
                                                                       Indels
            12887 MW; 9B4517648C121C5A CRC64;
                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Pror Natl: Acad. Sci. U.S.A. 99:16899-16903(2002).
                                           DB 1;
                                        79.3%; Score 504.5; DB
80.7%; Pred. No. 8e-43;
iive 9; Mismatches
                                                                                                                                                                                                                                                                                          05-JUL_2004 (TrEMBLrel. 27,
05-JUL_2004 (TrEMBLrel. 27,
05-JUL_2004 (TrEMBLrel. 27,
Hypothetical protein.
Mus musculus (Mouse).
                                                                       96; Conservative
                                                                                                                                                                                                                                                                 PRELIMINARY;
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115 1
115 AA;
                                          Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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NON TER
SEQUENCE
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Matches
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Q6PIP8
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SEQUENCE FROM N.A.

STRAIN=Czech II; TISSUE=Mammary tumor;

MEDLINE=228825; PubMed=12477932;

MEDLINE=228825; PubMed=12477932;

Altzueberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.C., Zeeberg B. Buercow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., WcKernan K.J., Malek J.A., Gunaratne P.H.,

Rack S.A., McEwan P.J., McKernan R.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M. K., Gibbs R.A.,

Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley N.C., Shevchenko Y., Boulfard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                        61 HYAESVKGRFTISRDDSKSAVYLQMTDLRTEDTGVYYCSRNYYGSTYDYWGQGTTLTVS 119
                                                                                                                                                                                                                                                                                                                                                              80 HYAESVKGRFTISRDDSKSRLYLQMSSLRAEDTGIYYCT-----NAMDYWGQGTSVTVS 133
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LD AAH31470
AC AAH31470;
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update.)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update.)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota Metazoa; Chordata; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                    20 EVKLEESGGGLVQPGGSMKLSCVASGFTFSNSWMNWVRQSPEKGLEWVAQIRLRSDNYAT
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                                                                                                                                 Gaps
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                                                                DB 2; Length 464;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Czech II; TISSUE=Mammary tumor;
Strausberg R.;
Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC0314770; AAH131470.1; -.
Hypothetical protein.
SEQUENCE 464 AA; 51246 MW; FDAC40A45B5E1443 CRC64;
51246 MW; FDAC40A45B5E1443 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                        Score 503.5; DB 2;
Pred. No. 4.9e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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79.8%; Pred. No. 4.9e-42;
iive 9; Mismatches 10
                                                         19.2%; Score 503.5; ilarity 79.8%; Pred. No. 4.9e Conservative 9; Mismatches
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Best Local Similarity 79.8°
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.
                           Query Match
Best Local Similarity
Best Socal Socal Similarity
   464 AA;
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RESULT 10
HV29_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 HYAESVKGRFTISRDDSKSAVYLQMTDLRTEDTGVYYCSRNYYGSTYDYWGQGTTLTV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Discensify 16:1170-1175(1977).

--- MISCELLANEOUS: This chain was isolated from a myeloma protein that binds inulin.

--- SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR, A90400; AVMSB7.

HSSP; P01810; 2FBJ.

InterPro; IPR007110; 1g-like.

InterPro; IPR003566; 1g-v.

PROMIT; SM00406; 1Gv.

PROMIT: PS0047; ig; 1.

SMART; SM00406; 1Gv.

PROMIT: PS00835; IG LIKE; 1.

Direct protein sequencing; Immunoglobulin V region.

DOMAIN

1 -> 13

19-like.
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Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).
-!- MISCELLANEOUS: This chain was isolated from a myeloma protein that binds inulin.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVKLEESGGGLVQPGGSMKLSCVASGFIFSNHWMNWVRQSPEKGLEWVAEIRSKSINSAT
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                                                                                                                                                                                                                                                                                                                 MEDLINE=77134726; PubMed=402936;
Vrana M., Rudikoff S., Potter M.;
"Heavy-chain variable-region sequence from an inulin-binding myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=78158406; PubMed=417344;
Vrana M., Rudikoff S., Potter M.;
"Sequence variation among heavy chains from inulin-binding myeloma
                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
1-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1g heavy chain V-III region U61.
1g heavy chain W-III region Cf.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.0%; Score 502.5; DB 1; Length 113; 81.4%; Pred. No. 1.2e-42; ive 7; Mismatches 10; Indels 5;
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                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
pleavy chain V-III region ABE-47N.
Mus musculus (Mouse).
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By similarity.
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HSSP, P01783; 1IGC.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96; Conservative
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                                               STANDARD;
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113 AA;
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                                             HV30 MOUSE
P01799;
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SEQUENCE
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P01797;
Matches
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                                                                                                                                                                                                                                                                                                61 HYAESVKGRFTISRDDSKSAVYLQMTDLRTEDTGVYYCSRNYYGSTYDYWGQGTTLTV 118
                                                                                                                                                                                                                                                                                                                  protein that
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01-OCT-1993 (Rel. 27, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ig heavy chain V-III region T957.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammallai, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1751.
1717—TaxID=10090;
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78.1%; Score 496.5; DB 1; Length 113;
Best Local Similarity 80.5%; Pred. No. 5e-42;
Matches 95; Conservative 7; Mismatches 11; Indels 5;
                                                                                                                                                                Score 499.5; DB 1; Length 113; Pred. No. 2.5e-42; 8; Mismatches 10; Indels 5.
                                                                                         1 >113 IG-like.
22 98 By similarity.
113 113
113 AA; 12671 MW; 76634C121C598285 CRC64;
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Direct protein sequencing; Immunoglobulin V region.
DOMAIN I >113 IG-like.
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By similarity.
                                                                                       Ig-like.
By similarity.
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MEDLINE=81216632; PubMed=6787122;
                                                                                                                                                                     78.5%;
80.5%;
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                       >113
98
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                                                                                                                                                  Query Match
Best Local Similarity
95; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                   HV31 MOUSE
P01800;
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RY PUBLINE=81216632; PubMed=6787122;
RA RUDLINE=81216632; PubMed=6787122;
RA Rudlkoff S., Potter M.;
Rudlkoff S., Potter M.;
Immunoglobulin heavy chains from anti-inulin myeloma proteins:
RT evidence for a new heavy chain joining segment.";
L. Immunol. 127:191-194(1981).
C. I- MISCELIANEOÚS: This chain was isolated from a myeloma protein that binds inulin.
C. I- SIMILARITY: Contains 1 immunoglobulin-like domain.
RT, A02073; HYMSAM.
RSP; P01783; HTGC.
C. I- SIMILARITY: Contains 1 immunoglobulin-like domain.
RSP; P01783; HTGC.
DR RSP; P01783; HTGC.
C. I- SIMILARITY: Contains 1 immunoglobulin V region.
DR RART; SMO440; IGV; 1.
DR RNART; RMO4406; IGV; 1.
DR RNART; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVKLEESGGGLVQPGRSMKLSCVASGFTFSNYMMWWVRQSPEKGLEWVAEIRLKSHNYAI 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 VKGRFTISRDDSKSSVYLQMNNLRAEDTGIYYCTR---PGVPDYWGQGTTLTVS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region AMPC1.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                     Length 111;
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113 AA; 12691 MW; 7A6D906AAA966E9E CRC64;
                                                                                                                                                                                                                                                       111 AA; 12304 MW; 0EDE98EC7348056A CRC64;
                                                                                                                                                                                                                                                                                                                                 Score 489; DB 1;
Pred. No. 2.8e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 83.3%; Pred. No. 2.8e es 95; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
Pfam; PF00047; ig; 1.
SMART; SW00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
IMMUNOGLODULIN V region.
DOWAIN <1 110
                                                                                                                                                                                                                                                                                                                                     76.98;
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HV01_RAT
ID HV01_RAT
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Bernard O., Gough N.M.;

Nuclectide sequence of immunoglobulin heavy chain joining segments

Nuclectide sequence of immunoglobulin heavy chain joining segments

Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).

-!- MISCELLANROUS: The sequence of the first 197 residues of the C

region was also determined and differs in only 3 positions from
the corresponding portion of the mouse MOPC 104e mu chain.

-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=78158406; PubMed=417344;
Vrana M., Rudikoff S., Potter M.;
"Sequence variation among heavy chains from inulin-binding myeloma
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 AA; 12647 MW; EESOF2F20EDB129B CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
pheavy chain V-III region HPC76 (Fragment).
                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-JUL-2004 (Rel. 44, Last annotation update)
19 heavy chain V-III region B109.
       113 AA
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By similarity.
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HSSP, P01852; INPD.
InterPro; IPR007110; Ig-like.
InterPro; IPR03596; Ig_v.
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STANDARD;
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HV29 MOUSE
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., McTewan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Morley B.M., Sodergren E.J., Lu X., Gibbs R.A.,
R. Helton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Nones S.J., Marra M.A.;
A Jones S.J., Marra M.A.;
T "Generation and initial analysis of more than 15,000 full-length human
RT and mouse CDNA sequences.";
R Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=mix FVB/N;
IISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 01, 1ast annotation update)
Ig heavy chain V region IR2 precursor.
Rattus norvegicus (Rat).
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NIBI_TAXID=10116;
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TISSUE-Mammary tumor. WAP-TGF alpha model. 7 months old;
MEDLINE-Z388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Mang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-83064537; PubMed-6222865;
Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;
"Structure and evolution of the heavy chain from rat immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 10:6041-6049(1982).

-!- MISCELLANEOUS: The mRNA was isolated from an IgE-secreting immunocytoma that arises spontaneously in LOU/C/WsL rats.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02075; EVRTR2.
--- FOLTR9; IMCP.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
PFAM; SM00406; Ig-v.
PFAM; PR0047; ig; 1.
PROSTTE; PS50835; IG_LKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.5%; Score 454.5; DB 1; Length 142; 68.9%; Pred. No. 1.1e-37; cive 17; Mismatches 18; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V region IR2. Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 AA; 16024 MW; DE29E6CFE745DF3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            479 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
hes 84; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 VS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VS 141
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SEQUENCE
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Matches
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Q7TMK4
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1 EVKLEESGGGLVQPGGSMKLSCVASGFIFSNHWMWVRQSPEKGLEWVAEIRSKSINSAT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 HYAESVKGRFTISRDDSKSAVYLOMTDLRTEDTGVYYCSRNYYGSTYDYWGQGTTLTVS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 YYSDSVKGRFTISRDDSKSGVYLQMNNLRPEDMGIYYCT----VEGMDYWGRGISVTVS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 EVKLDETGGGLVQPGRPMKLSCVASGFTFGDYWANWVRQSPEKGLEWVSQIRNKPYNYET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jamilus dromedarius (Dromedary) (Arabian camel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <code>TISSUE=Spleen;</code> Honda T., Akahori Y., Kurosawa Y.; Honda T., Akahori Y., Kurosawa Y.; Libraries of heavy-chain antibodies reflecting camel gamma2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                               69.7%; Score 443; DB 2; Length 47:
68.9%; Pred. No. 6.1e-36;
.ive 16; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gamma3 in vivo repertoires "; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AB092051; BAD00413.1; -;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                Pfam; PF007654; CI-8et; Z.
Pfam; PF00047; ig; 1.
PROSTTE; SMO0406; IGY; 1.
PROSTTE; PS08315; IG_LIKE; 4.
PROSTTE; PS08209; IG_MHC; UNKNOWN_2.
HYPOCHELICAI protein.
SEQUENCE 479 AA; 52209 MW; 532DED9D46D0AEED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 121
121 AA; 12867 MW; 34F0EB03C2404119 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAD00413;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Immunoglobulin heavy chain VHDJ region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.2%; Score 421; DB 2;
65.5%; Pred. No. 2.1e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
         Submitted (AUG-2001) ...

MRI, BCO55905, AAH55905.1; -.

InterPro; IPR007110; Ig-11ke.

InterPro; IPR003597; Ig cl.

InterPro; IPR003596; Ig MHC.

InterPro; IPR003596; Ig V.
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us-09-897-724-5.rup
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2; Gaps 1;
             Matches 78; Conservative 17; Mismatches 22; Indels
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